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(54) Title: METHOD FOR ISOLATING HEPATITIS C VIRUS PEPTIDES

(57) Abstract: Described is a method for isolating Hepatitis C Virus peptides (HPs) which have a binding capacity to a MHC/HLA molecule or a complex comprising said HCV-peptide and said MHC/HLA molecule characterized by the following steps: - providing a pool of HCV-peptide, said pool containing HCV-peptides which bind to said MHC/HLA molecule and HCV-peptides which do not bind to said MHC/HLA molecule, -contacting said MHC/HLA molecule with said pool of HCV-peptides whereby a HCV-peptide which has a binding capacity to said MHC/HLA molecule binds to said MHC/HLA molecule and a complex comprising said HCV-peptide and said MHC/HLA molecule is formed, -detecting and optionally separating said complex from the HCV-peptide which do not bind to said MHC/HLA molecule and optionally isolating and characterising the HCV-peptide from said complex.

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Method for Isolating Hepatitis C Virus Peptides

The present invention relates to a method for isolating HCV-peptides, especially for isolating HCV T cell epitopes which have a binding capacity to a MHC/HLA molecule.

The immune system is a complex network of inter-related cell types and molecules, which has evolved in order to protect multicellular organisms from infectious microorganisms. It can be divided into the evolutionary older innate (or natural) immunity and adaptive (or acquired) immunity. The innate immune system recognizes patterns, which are usually common and essential for pathogens. For this limited number of molecular structures germline encoded receptors have evolved. By contrast, cells of the adaptive immune system - B and T lymphocytes - can recognize a huge variety of antigenic structures. The receptors, termed according to the cell types expressing them, B cell receptor (BCR, its soluble versions are called antibodies) and T cell receptor (TCR, only cell-surface associated forms) are generated by somatic recombination and show a clonal distribution. Thus, initially there is only small number of cells with a certain specificity. Upon antigen encounter these cells start to divide (clonal expansion) to generate an effector population able to cope with the antigen. After elimination of antigen a specialized sub-population of cells specifically recognizing this antigen remains as immunological memory. Taken together the adaptive immune system is slow (compared to innate immunity), however specific and it improves upon repeated exposure to a given pathogen/antigen.

T cells have a central role in adaptive immunity. Their receptors (TCRs) recognize "major histocompatibility complex" (MHC or HLA):peptide complexes on the surface of cells. These peptides are called T cell epitopes and represent degradation products of antigens. There are two major classes of T cells: CD8-positive cytotoxic T cells (CTL) are restricted to MHC class I. CD4-positive helper T cells (HTL) are restricted to MHC class II. HTL are essential for many features of adaptive immunity: activation of so called "professional antigen-presenting cells" (APCs), immunoglobulin (Ig) class switch, the germinal center reaction and

Ig affinity maturation, activation of CTL, immunological memory, regulation of the immune response and others.

MHC molecules collect peptides inside the cell and present them on the cell surface to TCRs of T cells. There are two major classes of MHC, class I recognized by CD8-positive CTL and class II recognized by CD4-positive HTL.

MHC class I molecules consist of a membrane-anchored alpha-chain of 45 kDa and the non-covalently attached b2-microglobulin (b2m) of 12 kDA. Resolution of the 3-dimensional structure by X-ray crystallography (Stern and Wiley 1994) revealed that the alpha-chain possesses a cleft, which is closed at both ends and accommodates peptides from 8 to 11 amino acids length. Class I molecules are ubiquitously expressed, and the peptides they present originate from cytoplasmic proteins. These are degraded by the proteasome, and the resulting peptides are actively transported into the endoplasmatic reticulum (ER). There, with the help of several chaperones, MHC:peptide complexes are formed and transported to the cell surface (Heemels 1995). Thus, MHC class I mirrors the proteome of a cell on its surface and allows T cells to recognize intracellular pathogens or malignant cells.

MHC class II molecules consist of two membrane-anchored proteins (alpha- and beta-chain) of 35 kDa and 30 kDa, respectively. These together form a cleft, open at both ends, which can accommodate peptides of variable length, usually from 12 to 25 amino acids. Despite these differences, class I and II molecules share surprising structural similarity (Stern and Wiley 1994). Class II molecules are only expressed on professional APC including dendritic cells (DC), B-cells and macrophages/monocytes. These cells are specialized in taking up and processing antigens in the endosomal pathway. Immediately after their biosynthesis, class II molecules are complexed by the so-called invariant chain (Ii), which prevents binding of peptides in the ER. When vesicles containing class II:Ii complexes fuse with endosomes containing degradation products of exogenous antigen, Ii is degraded until the MHC binding cleft is only complexed by the so-called CLIP peptide. The latter is with the help of chaperones like HLA-DM exchanged by antigenic peptides (Villadangos 2000).

Finally, MHC:peptide complexes are again presented on the surface of APCs, which interact in numerous ways with HTL.

Being both polygenic and extremely polymorphic, the MHC system is highly complex. For the class I alpha-chain in humans there are three gene loci termed HLA-A, -B and -C. Likewise, there are three class II alpha-chain loci (DRA, DQA, DPA); for class II beta-chain loci the situation is even more complex as there are four different DR beta-chains (DRB1,2,3,5) plus DQB and DPB. Except the monomorphic DR alpha-chain DRA, each gene locus is present in many different alleles (dozens to hundreds) in the population (Klein 1986). Different alleles have largely distinct binding specificities for peptides. Alleles are designated, for example, HLA-A*0201 or HLA-DRB1*0401 or HLA-DPA*0101/DPB*0401.

T cell epitopes have been identified by a variety of approaches (Van den Eynde 1997). T cell lines and clones have for instance been used to screen cDNA expression libraries for instance in the context of COS cells transfected with the appropriate HLA-molecule. Alternatively, biochemical approaches have been pursued. The latter involved elution of natural ligands from MHC molecules on the surface of target cells, the separation of these peptides by several chromatography steps, analysis of their reactivity with lymphocytes in epitope reconstitution assays and sequencing by mass spectrometry (Wölfel et al. 1994, Cox et al. 1994).

Recently the advent of highly sensitive cytokine detection assays like the IFN-gamma ELIspot allowed using lymphocytes directly ex vivo for screening of overlapping synthetic peptides (Maecker 2001, Kern 2000, Tobery 2001). Primarily, Kern et al. (1999&2000) used arrays of pools of overlapping 9mer peptides to map CD8+ T cell epitopes in vitro. Later, Tobery et al., 2001 modified this approach and demonstrated that pools containing as many as 64 20mer peptides may be used to screen for both CD8+ and CD4+ T cell epitopes in mice. Both these methods were based on the monitoring of antigen-specific response by measuring INF-gamma production either by intracellular staining (Kern et al 2000) or in ELIspot assay (Tobery et al., 2001). By use of mixtures of 15-mers the CD4+ T cell responses are approximately

equal to those detected when whole soluble protein was used as an antigen, while -not surprising- the CD8+ T cell responses are significantly higher than the often negligible responses detected with soluble protein stimulation. Furthermore, the CD8+ T cell responses to a mixture of 15 amino acid peptides are similar to those obtained with a mix of 8-12 amino acid peptides, selected to represent known MHC class I minimal epitopes. Most probably peptidases associated with the cell membrane are responsible for "clipping" peptides to optimal length under these circumstances (Maecker et al, 2001).

An interesting alternative is to screen synthetic combinatorial peptide libraries with specific lymphocytes. For instance, a decapeptide library consisting of 200 mixtures arranged in a positional scanning format, has been successfully used for identification of peptide ligands that stimulate clonotypic populations of T cells (Wilson, et al., J. Immunol., 1999, 163:6424-6434).

Many T cell epitopes have been identified by so called "Reverse immunological approaches" Rammensee 1999). In this case the protein giving rise to a potential T cell epitope is known, and its primary sequence is scanned for HLA binding motifs. Typically dozens to hundreds of candidate peptides or even a full set of overlapping peptides are synthesized and tested for binding to HLA molecules. Usually, the best binders are selected for further characterization with regard to their reactivity with T cells. This can for instance be done by priming T cells in vitro or in vivo with the help of HLA transgenic mice.

Hepatitis C Virus (HCV) is a member of the flaviviridiae chronically infecting about 170 million people worldwide. There are at least 6 HCV genotypes and more than 50 subtypes have been described. In America, Europe and Japan genotypes 1, 2 and 3 are most common. The geographic distribution of HCV genotypes varies greatly with genotype 1a being predominant in the USA and parts of Western Europe, whereas 1b predominates in Southern and Central Europe (Bellentani 2000).

HCV is transmitted through the parenteral or percutan route, and

replicates in hepatocytes. About 15% of patients experience acute self-limited hepatitis associated with viral clearance and recovery. About 80% of infected persons become chronic carriers. Infection often persists asymptomatically with slow progression for years, however ultimately HCV is a major cause of cirrhosis, end-stage liver disease and liver cancer (Liang 2000). Strength and quality of both HTL and CTL responses determine whether patients recover (spontaneously or as a consequence of therapy) or develop chronic infection (Liang 2000).

Standard therapy of HCV comprises a combination of pegylated interferon-alpha and the antiviral ribavirin. Virologic responses are, depending on the genotype, achieved in about 50% of HCV patients. The low tolerability and the considerable side effects of this therapy clearly necessitate novel therapeutic intervention including therapeutic vaccines (Cornberg 2002). However, presently the detailed understanding of which epitopes in which MHC combination lead to successful immune responses is lacking (Ward 2002). Therefore, a comprehensive analysis of the T-cell response against the entire HCV is required for development of therapeutic epitope-based vaccines.

The HCV virion contains a 9.5-kilobase positive single-strand RNA genome encoding a large single polyprotein of about 3000 amino acids. The latter is processed to at least 10 proteins by both host and HCV-enoded proteolytic activities (Liang 2000). Importantly, the HCV RNA-dependent RNA polymerase is error prone giving rise to the evolution of viral quasispecies and contributing to immune-escape variants (Farci 2000).

It is an object of the present invention to provide a method for screening HCV-peptides for specific MHC molecules, preferably for delivering suitable and specific HCV T cell epitopes selected from a variety of HCV-peptides having unknown specificity for a given MHC molecule and thereby to provide efficient means for preventing and combatting HCV infections.

Therefore the present invention provides a method for isolating HCV-peptides which have a binding capacity to a MHC/HLA molecule or a complex comprising said HCV-peptide and said MHC/HLA mo-

lecule which method comprises the following steps:

-providing a pool of HCV-peptides, said pool containing HCV-peptides which bind to said MHC/HLA molecule and HCV-peptides which do not bind to said MHC/HLA molecule,

-contacting said MHC/HLA molecule with said pool of HCV-peptides whereby a HCV-peptide which has a binding capacity to said MHC/HLA molecule binds to said MHC/HLA molecule and a complex comprising said HCV-peptide and said MHC/HLA molecule is formed,

-detecting and optionally separating said complex from the HCV-peptides which do not bind to said MHC/HLA molecule and

-optionally isolating and characterising the HCV-peptide from said complex.

The present invention also provides a method for isolating HCV T cell epitopes which have a binding capacity to a MHC/HLA molecule or a complex comprising said epitope and said MHC/HLA molecule which method comprises the following steps:

-providing a pool of HCV-peptides, said pool containing HCV-peptides which bind to a MHC/HLA molecule and HCV-peptides which do not bind to said MHC/HLA molecule,

-contacting said MHC/HLA molecule with said pool of HCV-peptides whereby a HCV-peptide which has a binding capacity to said MHC/HLA molecule binds to said MHC/HLA molecule and a complex comprising said HCV-peptide and said MHC/HLA molecule is formed,

-detecting and optionally separating said complex from the HCV-peptides which do not bind to said MHC/HLA molecule,

-optionally isolating and characterising the HCV-peptide from said complex,

-assaying said optionally isolated HCV-peptide or said complex in a T cell assay for T cell activation capacity and

-providing the optionally isolated HCV-peptide with a T cell activation capacity as HCV T cell epitope or as complex.

The method according to the present invention enables a screening system for screening binding capacity to specific MHC/HLA molecules. Identifying MHC binding molecules is an important tool for molecular characterisation of pathogens, tumors, etc. It is therefore possible with the present invention to screen a

variety (a "pool") of potential HCV-peptides as ligands at once for their functional affinity towards MHC molecules. Binding affinity towards MHC molecules is also a necessary prerequisite for HCV-peptides intended to be used as T cell epitopes, although not a sufficient one. Suitable HCV T cell epitope candidates have also to be screened and assayed with respect to their T cell activation capacity. The combination of the screening method for binding according to the present invention with a suitable T cell assay therefore provides the method for isolating HCV T cell epitopes according to the present invention wherein such T cell epitopes are identifiable out of a pool of potential HCV-peptides using an MHC binding assay.

In contrast to the prior art, where such assays have always been performed on ligands with known binding/MHC specificity, the methods according to the present invention provide such assays as a screening tool for pools with ligands of unknown specificity. In the prior art such assays have been typically performed on individual single ligands, to test their binding affinity to MHC/HLA molecules. In Kwok et al. (2001) pools of maximally up to 5 overlapping synthetic peptides were used to generate MHC class II tetramers; the latter were then used to stain PBMC for T cells specific for particular MHC class II:peptide complexes which were generated in the binding reaction with the pools of 5 peptides. However, an increase in the number of ligands per pool in such an approach was not regarded as being possible, both for sensitivity and specificity reasons (Novak et al. 2001). A problem with regard to specificity would be the generation of MHC tetramers with more then one binder per tetramer, if more than one binder would be present in the pool. This would preclude staining of T cells, which is used for identification of epitopes in the approach described in the prior art. In strong contrast to that the approach according to the present invention allows the identification of more than on binder out of highly complex mixtures containing more than one binder.

The nature of the pool to be screened with the present invention is not critical: the pools may contain any naturally or not naturally occurring HCV-peptide which a) binds specifically to

MHC/HLA molecules and/or b) may be specifically recognized by T cells. The binding properties of the set of HCV-peptides of the pool with respect to MHC molecules is not known; therefore, usually binders and at least a non-binder for a given MHC molecule are contained in the pool. The pool therefore comprises at least ten different HCV-peptides. Practically, pools are used according to the present invention containing significantly more different HCV-peptide species, e.g. 20 or more, 100 or more, 1.000 or more or 10.000 or more. It is also possible to screen larger libraries (with e.g. more than 10^6, more than 10^8 or even more than 10^{10} different HCV-peptide species). This, however, is mainly dependent on the availability of such HCV-peptide libraries.

Preferred pools of ligands to be used in the method according to the present invention are selected from the group consisting of a pool of peptides, especially overlapping peptides, a pool of protein fragments, a pool of modified peptides, a pool obtained from antigen-presenting cells, preferably in the form of total lysates or fractions thereof, especially fractions eluted from the surface or the MHC/HLA molecules of these cells, a pool comprised of fragments of cells, especially HCV containing cells, tumor cells or tissues, especially from liver, a pool comprised of peptide libraries, pools of (poly)-peptides generated from recombinant DNA libraries, especially derived from pathogens or (liver) tumor cells, a pool of proteins and/or protein fragments from HCV or mixtures thereof.

The HCV-peptides of the pools may be derived from natural sources (in native and/or derivatised form) but also be produced synthetically (e.g. by chemical synthesis or by recombinant technology). If (poly)peptide ligands are provided in the pools, those peptides are preferably generated by peptide synthesizers or by recombinant technology. According to a preferred embodiment, a pool of (poly)peptides may be generated from recombinant DNA libraries, e.g. derived from HCV or HCV containing (tumor) cells, by in vitro translation (e.g. by ribosome display) or by expression through heterologous hosts like E.coli or others.

The nature of the specific MHC molecules (of course also MHC-

like molecules are encompassed by this term) to be selected for the present methods is again not critical. Therefore, these molecules may be selected in principle from any species, especially primates like humans (HLA, see below), chimpanzees, other mammals, e.g. maquaques, rabbits, cats, dogs or rodents like mice, rats, guinea pigs and others, agriculturally important animals like cattle, horses, sheep and fish, although human (or "humanized") molecules are of course preferred for providing vaccines for humans. For providing vaccines for specific animals, especially agriculturally important animals, like cattle, horses, sheep and fish, the use of MHC molecules being specific for these animals is preferred.

Preferred HLA molecules therefore comprise Class I molecules derived from the HLA-A, -B or- C loci, especially A1, A2, A3, A24, A11, A23, A29, A30, A68; B7, B8, B15, B16, B27, B35, B40, B44, B46, B51, B52, B53; Cw3, Cw4, Cw6, Cw7; Class II molecules derived from the HLA-DP, -DQ or -DR loci, especially DR1, DR2, DR3, DR4, DR7, DR8, DR9, DR11, DR12, DR13, DR51, DR52, DR53; DP2, DP3, DP4; DQ1, DQ3, DQ5, DQ6; and non-classical MHC/HLA and MHC/HLA-like molecules, which can specifically bind ligands, especially HLA-E, HLA-G, MICA, MICB, Qa1, Qa2, T10, T18, T22, M3 and members of the CD1 family.

According to a preferred embodiment, the methods according to the present invention is characterised in that said MHC/HLA molecules are selected from HLA class I molecules, HLA class II molecules, non classical MHC/HLA and MHC/HLA-like molecules or mixtures thereof, or mixtures thereof.

Preferably, the optional characterising step of the HCV-peptides of the complex is performed by using a method selected from the group consisting of mass spectroscopy, polypeptide sequencing, binding assays, especially SDS-stability assays, identification of ligands by determination of their retention factors by chromatography, especially HPLC, or other spectroscopic techniques, especially violet (UV), infra-red (IR), nuclear magnetic resonance (NMR), circular dichroism (CD) or electron spin resonance (ESR), or combinations thereof.

According to a preferred embodiment the method of the present invention is characterised in that it is combined with a cytokine secretion assay, preferably with an Elispot assay, an intracellular cytokine staining, FACS or an ELISA (enzyme-linked immunoassays) (see e.g. Current Protocols in Immunology).

Preferred T cell assays comprise the mixing and incubation of said complex with isolated T cells and subsequent measuring cytokine secretion or proliferation of said isolated T cells and/or the measuring up-regulation of activation markers, especially CD69, CD38, or down-regulation of surface markers, especially CD3, CD8 or TCR and/or the measuring up-/down-regulation of mRNAs involved in T cell activation, especially by real-time RT-PCR (see e.g. Current Protocols in Immunology, Current Protocols in Molecular Biology).

Further preferred T cell assays are selected from T cell assays measuring phosphorylation/de-phosphorylation of components downstream of the T cell receptor, especially p56 lck, ITAMS of the TCR and the zeta chain, ZAP70, LAT, SLP-76, fyn, and lyn, T cell assays measuring intracellular Ca^{++} concentration or activation of Ca^{++}-dependent proteins, T cell assays measuring formation of immunological synapses, T cell assays measuring release of effector molecules, especially perforin, granzymes or granulolysin or combinations of such T cell assays (see e.g. Current Protocols in Immunology, Current Protocols in Cell Biology).

In order to identify the molecular determinants of immune-protection against HCV a specific method of epitope capturing was applied using synthetic peptides representing the conserved parts of HCV genotypes 1, 2 and 3. Focusing on conserved regions ensures broad applicability of the epitopes. Moreover, these regions probably cannot easily be mutated by the virus, thus minimizing the danger of evolution of immune-escape variants.

With the methods of the present invention novel HCV-epitopes are detected. According to a further aspect, the present invention therefore also provides HCV T cell epitopes identifiable by a method according to the present invention, said T cell epitopes preferably being selected from the group consisting of poly-

peptides comprising the peptides A120-A124, B25-B30, B46-B48, B84-B92, C106, C113-C114, 1627, 1628, 1629, 1604 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0101, *0401, *0404, *0701 and thus covering at least 45-55% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides 1630, C97, 1547, B94-B98, A272-A276 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0101, *0401, *0701 and thus covering at least 40-50% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides B120, B122, C108, C134, C152 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0101, *0404, *0701 and thus covering at least 45% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides 1606, 1607, 1577, 1578 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0401, *0404, *0701 and thus covering at least 45% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides B50-52, 1623, C130 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0101, *0401, *0404 and thus covering at least 40% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides 1603, C96 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0101, *0701 and thus covering at least 40% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides C191 according to Table 1, being a novel ligand for at least HLA-DRB1*0401, *0701 and thus covering at least 40% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides A216-A224, A242-A244, C92-C93 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0101, *0401 and thus covering at least 35% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptide A174 according to Table 1 or 2, being a novel ligand for at least HLA-DRB1*0404, *0701 and thus covering at least 25-30% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides B32-B38, B100-B102, C135 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0101, *0404 and thus covering at least 20-25% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptide C162 according to Table 1 or 2, being a novel ligand for at least HLA-DRB1*0401, *0404 and thus covering at least 20-25% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides 1618, 1622, 1624, 1546, 1556 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0701 and thus covering at least 25% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides A114, B58, B112-B118, B18-B22, C112, C116, C122, C127, C144, C159-C160, C174, 1558, 1581 according to Table 1 or 2. These peptides are novel ligands for at least HLA-DRB1*0101 and thus covering at least 20% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptide C95, being a novel ligand for at least HLA-DRB1*0401 and thus covering at least 20% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides C129, C157-C158, A254-A258, 1605, C109, C161 according to Table 1 or 2. These peptides comprising novel ligands for at least HLA-DRB1*0404 and thus covering at least 5% of major populations (see Tab. 2).

Preferred polypeptides are selected from the group comprising the peptides 1547, 1555, 1558, 1559, 1560, 1563, 1592, 1604, 1605, 1616, 1621, 1623, 1625, 1627, 1630, 1649, 1650, 1651, 1652, 1654, 1655, 1656 according to Table 1 or 2, these peptides displaying immunogenicity in HLA-DRB1*0401 transgenic mice (see Example II) and thus representing or containing a confirmed HLA class II T-cell epitope binding to at least HLA-DRB1*0401 (see Tab. 3).

Preferred polypeptides are selected from the group comprising the peptides 1545, 1552, 1555, 1558, 1559, 1560, 1577, 1592, 1604, 1605, 1615, 1617, 1621, 1627, 1631, 1632, 1641, 1647, 1650, 1651, 1652, 1653, 1654, 1655 according to Table 1 or 2, these peptides displaying immunogenicity in HLA-A*0201 transgenic mice (see Example II) and thus representing or containing a confirmed HLA class I T-cell epitope binding to at least HLA-A*0201 (see Tab. 3).

Preferred polypeptides which are shown to be HLA-B*0702 epitopes with T-cell activating capacity are selected from the group consisting of polypeptides 1506, 1526, 1547, 1552, 1553, 1555, 1558, 1562, 1563, 1565, 1577, 1578, 1580, 1587, 1592, 1604, 1605, 1621, 1623, 1624, 1627, 1628, 1647, 1650, 1651, 1843 with sequence LPRRGPRL (contained in 1506) and 1838 with sequence SPGALVVGVI (contained in 1587) as minimal HLA-B*0702 epitopes.

Peptides 1526, 1565, 1631 are also shown to be immunogenic in HLA-DRB1*0401 transgenic mice contain known class II epitopes. Peptides 1526, 1553, 1565, 1587, 1623, 1630 are also shown to be immunogenic in HLA-A*0201 transgenic mice contain known A2 epitopes.

Preferred polypeptides are selected from the group comprising

the peptides listed in tables 3, 5 and the bold peptides in 7 ("hotspots").

The preferred polypeptides mentioned above also include all fragments containing the minimal sequence of the epitope, i.e. the 8- or 9-mer being necessary for binding to MHC/HLA molecules.

Preferably, the epitopes or peptides according to the present invention further comprises 1 to 30, preferably 2 to 10, especially 2 to 6, naturally occurring amino acid residues at the N-terminus, the C-terminus or at the N- and C-terminus. For the purposes of the present invention the term "naturally occurring" amino acid residue relates to amino acid residues present in the naturally occurring protein at the specific position, relative to the epitope or peptide. For example, for the HLA-A2 epitope with the amino acid sequence HMWNFISGI contained within peptide ID 1565 (Tab. 1), the naturally occurring amino acid residue at the N-terminus is -K; the three naturally occurring amino acid residues at the C-terminus are -QYL. A "non-naturally occurring" amino acid residue is therefore any amino acid residue being different as the amino acid residue at the specific position relative to the epitope or peptide.

According to a preferred embodiment of the present invention, the present epitopes or peptides further comprise non-naturally occurring amino acid(s), preferably 1 to 1000, more preferred 2 to 100, especially 2 to 20 non-naturally occurring amino acid residues, especially at the N-terminus, the C-terminus or at the N- and C-terminus. Also combinations of non-naturally and naturally occurring amino acid residues are possible under this specific preferred embodiment. The present epitope may also contain modified amino acids (i.e. amino acid residues being different from the 20 "classical" amino acids, such as D-amino acids or S-S bindings of Cys) as additional amino acid residues or in replacement of a naturally occurring amino acid residue.

It is clear that also epitopes or peptides derived from the present epitopes or peptides by amino acid exchanges improving, conserving or at least not significantly impeding the T cell ac-

tivating capability of the epitopes are covered by the epitopes or peptides according to the present invention. Therefore, the present epitopes or peptides also cover epitopes or peptides, which do not contain the original sequence as derived from a specific strain of HCV, but trigger the same or preferably an improved T cell response. These epitopes are referred to as "heteroclitic". These include any epitope, which can trigger the same T cells as the original epitope and has preferably a more potent activation capacity of T cells preferably in vivo or also in vitro. Also the respective homologous epitopes from other strains of HCV are encompassed by the present invention.

Heteroclitic epitopes can be obtained by rational design i.e. taking into account the contribution of individual residues to binding to MHC/HLA as for instance described by Ramensee et al. 1999 or Sturniolo et al. 1999, combined with a systematic exchange of residues potentially interacting with the TCR and testing the resulting sequences with T cells directed against the original epitope. Such a design is possible for a skilled man in the art without much experimentation.

Another possibility includes the screening of peptide libraries with T cells directed against the original epitope. A preferred way is the positional scanning of synthetic peptide libraries. Such approaches have been described in detail for instance by Blake et al 1996 and Hemmer et al. 1999 and the references given therein.

As an alternative to epitopes represented by the cognate HCV derived amino acid sequence or heteroclitic epitopes, also substances mimicking these epitopes e.g. "peptidemimetica" or "retro-inverso-peptides" can be applied.

Another aspect of the design of improved epitopes is their formulation or modification with substances increasing their capacity to stimulate T cells. These include T helper cell epitopes, lipids or liposomes or preferred modifications as described in WO 01/78767.

Another way to increase the T cell stimulating capacity of epi-

topes is their formulation with immune stimulating substances for instance cytokines or chemokines like interleukin-2, -7, -12, -18, class I and II interferons (IFN), especially IFN-gamma, GM-CSF, TNF-alpha, flt3-ligand and others.

According to a further aspect, the present invention is drawn to the use of a HCV epitope or HCV peptide according to the present invention for the preparation of a HLA restricted vaccine for treating or preventing hepatitis C virus (HCV) infections.

The invention also encompasses the use of an epitope according to the present invention for the preparation of a vaccine for treating or preventing preventing hepatitis C virus (HCV) infections.

Consequently, the present invention also encompasses a vaccine for treating or preventing hepatitis C virus (HCV) infections comprising an epitope according to the present invention.

Furthermore, also a HLA specific vaccine for treating or preventing hepatitis C virus (HCV) infections comprising the epitopes or peptides according to the present invention is an aspect of the present invention.

Preferably, such a vaccine further comprises an immunomodulating substance, preferably selected from the group consisting of polycationic substances, especially polycationic polypeptides, immunomodulating nucleic acids, especially deoxyinosine and/or deoxyuracile containing oligodeoxynucleotides, or mixtures thereof.

Preferably the vaccine further comprises a polycationic polymer, preferably a polycationic peptide, especially polyarginine, polylysine or an antimicrobial peptide.

The polycationic compound(s) to be used according to the present invention may be any polycationic compound, which shows the characteristic effect according to the WO 97/30721. Preferred polycationic compounds are selected from basic polypeptides, organic polycations, basic polyaminoacids or mixtures thereof.

These polyaminoacids should have a chain length of at least 4 amino acid residues. Especially preferred are substances containing peptidic bounds, like polylysine, polyarginine and polypeptides containing more than 20%, especially more than 50% of basic amino acids in a range of more than 8, especially more than 20, amino acid residues or mixtures thereof. Other preferred polycations and their pharmaceutical compositions are described in WO 97/30721 (e.g. polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 amino acid residues, especially between 30 and 200 residues.

These polycationic compounds may be produced chemically or recombinantly or may be derived from natural sources.

Cationic (poly)peptides may also be polycationic anti-bacterial microbial peptides. These (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically or recombinantly. Peptides may also belong to the class of defensines. Such host defense peptides or defensines are also a preferred form of the polycationic polymer according to the present invention. Generally, a compound allowing as an end product activation (or down-regulation) of the adaptive immune system, preferably mediated by APCs (including dendritic cells) is used as polycationic polymer.

Especially preferred for use as polycationic substance in the present invention are cathelicidin derived antimicrobial peptides or derivatives thereof (WO 02/13857), incorporated herein by reference), especially antimicrobial peptides derived from mammal cathelicidin, preferably from human, bovine or mouse, or neuroactive compounds, such as (human) growth hormone (as described e.g. in WO01/24822).

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin, especially mouse, bovine or especially human cathelins and/or

cathelicidins. Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20 amino acid residues. Derivations may include the substitution or modification of the natural amino acids by amino acids, which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen/vaccine composition according to the present invention. However, these cathelin molecules surprisingly have turned out to be also effective as an adjuvant for a antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further immunactivating substances.

Another preferred polycationic substance to be used according to the present invention is a synthetic peptide containing at least 2 KLK-motifs separated by a linker of 3 to 7 hydrophobic amino acids, especially L (WO 02/32451, incorporated herein by reference).

The immunomodulating (or:immunogenic) nucleic acids to be used according to the present invention can be of synthetic, prokaryotic and eukaryotic origin. In the case of eukaryotic origin, DNA should be derived from, based on the phylogenetic tree, less developed species (e.g. insects, but also others). In a preferred embodiment of the invention the immunogenic oligodeoxynucleotide (ODN) is a synthetically produced DNA-molecule or mixtures of such molecules. Derivatives or modifications of ODNs such as thiophosphate substituted analogues (thiophosphate residues substitute for phosphate) as for example described in US patents US 5,723,335 and US 5,663,153, and other derivatives and modifications, which preferably stabilize the immunostimulatory composition(s) but do not change their immunological properties, are also included. A preferred sequence motif is a six base DNA motif containing an (unmethylated) CpG dinucleotide flanked by two 5' purines and two 3' pyrimidines (5'-Pur-Pur-C-G-Pyr-Pyr-3'). The CpG motifs contained in the ODNs according to the present invention are more common in microbial than higher vertebrate DNA and display differences in the pattern of methyl-

ation. Surprisingly, sequences stimulating mouse APCs are not very efficient for human cells. Preferred palindromic or non-palindromic ODNs to be used according to the present invention are disclosed e.g. in Austrian Patent applications A 1973/2000, A 805/2001, EP 0 468 520 A2, WO 96/02555, WO 98/16247, WO 98/18810, WO 98/37919, WO 98/40100, WO 98/52581, WO 98/52962, WO 99/51259 and WO 99/56755 all incorporated herein by reference. Apart from stimulating the immune system certain ODNs are neutralizing some immune responses. These sequences are also included in the current invention, for example for applications for the treatment of autoimmune diseases. ODNs/DNAs may be produced chemically or recombinantly or may be derived from natural sources. Preferred natural sources are insects.

Alternatively, also nucleic acids based on inosine and cytidine (as e.g. described in the WO 01/93903) or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448; incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention.

Of course, also mixtures of different immunogenic nucleic acids may be used according to the present invention.

Preferably, the present vaccine further comprises a pharmaceutically acceptable carrier.

According to a further preferred embodiment, the present vaccine comprises an epitope or peptide which is provided in a form selected from peptides, peptide analogues, proteins, naked DNA, RNA, viral vectors, virus-like particles, recombinant/chimeric viruses, recombinant bacteria or dendritic cells pulsed with protein/peptide/RNA or transfected with DNA comprising the epitopes or peptides.

According to a further aspect, the present invention is drawn to T cells, a T cell clone or a population (preparation) of T cells specifically recognizing any HCV epitope or peptide according to the present invention, especially a HCV epitope as described above. A preferred application of such T cells is their expan-

sion in vitro and use for therapy of patients e.g. by adoptive transfer. Therefore, the present invention also provides the use of T cells, a T cell clone or a population (preparation) of T cells for the preparation of a composition for the therapy of HCV patients.

Such T cells (clones or lines) according to the present invention, specifically those recognizing the aforementioned HCV peptides are also useful for identification of heteroclitic epitopes, which are distinct from the originally identified epitopes but trigger the same T cells.

Such cells, compositions or vaccines according to the present invention are administered to the individuals in an effective amount.

According to a further aspect, the present invention also relates to the use of the peptides with formulae QRKTKRNTN, QRKTKRNT, or 1615, 1616, 1617 in particular 9meric peptides derived from the latter 3 peptides with formulae SAKSKFGYG, SAKSKYGYG, or SARSKYGYG as HLA-B*08 epitopes, especially for the preparation of a pharmaceutical preparation for a HLA-B*08 specific vaccine; the use of the peptides with the formulae RKTKRNTNR as HLA-B*2705 epitope, especially for the preparation of a pharmaceutical preparation for a HLA-B*2705 specific vaccine; and the use of the peptides with the formulae ARLIVFPDL as HLA-B*2705 and HLA-B*2709 specific vaccine. Further, it also relates to the use of the hotspot epitopes selected from the group of peptides 1835, 84EX, 87EX, 89EX, 1426, 1650, 1836, 1846, 1651, 1800, 1799, C114, 1827, C112, C114EX, 1827EX, 1798, 1604, 1829, 1579, 1624, 1848, 1547, A1A7, A122EX, A122, 1825, A241, B8B38, C70EX, C92, C97, C106, and C134 according to table 7 for the preparation of a vaccine comprising synthetic peptides, recombinant protein and/or DNA constitutes of such epitopes.

In particular, two or more epitope hotspots can be combined, with or without linker sequences. Preferred linker sequences consist for instance of 3 to 5 glycine, or alanine or lysine residues. This may be achieved by peptide synthesis, However, combination of hotspots may result in quite long polypeptides.

In this case, cloning DNA encoding for such constructs and expressing and purifying the corresponding recombinant protein is an alternative. Such recombinant proteins can be used as antigens, which in combination with the right adjuvant (IC31, pR,...) can elicit T-cell responses against all the epitopes they harbor. At the same time, such artificial polypeptides are devoid of the activities (enzymatic, toxic, immuno-suppressive, ...), the natural HCV antigens may possess.

There are several other ways of delivering T-cell epitope hotspots or combinations thereof. These include: recombinant viral vectors like vaccinia virus, canary pox virus, adenovirus; self-replicating RNA vectors; "naked DNA" vaccination with plasmids encoding the hotspots or combination thereof; recombinant bacteria (e.g. Salmonella); dendritic cells pulsed with synthetic peptides, or recombinant protein, or RNA or transfected with DNA, each encoding T-cell epitope hotspots or combinations thereof.

The invention will be explained in more detail by way of the following examples and drawing figures, to which, however it is not limited.

Fig.1 shows 40 peptide mixtures each containing up to 20 HCV derived 15- to 23mer peptides.

Fig.2 shows the Epitope Capture approach using peptide pools and empty DRB1*0401 molecules.

Fig.3 shows the Epitope Capture approach using peptide pools and empty DRB1*0404 molecules.

Fig.4 shows binding of individual peptides to DRB1*0401.

Fig.5 shows binding of individual peptides to DRB1*0404.

Fig.6 shows binding of individual peptides to DRB1*0101.

Fig.7 shows peptides binding to DRB1*0701.

Fig.8 shows mouse IFN-gamma ELIspot with splenocytes or separated CD8+ or CD4+ cells from HLA-DRB1*0401 tg mice vaccinated with Ipep1604+IC31.

Fig.9 shows mouse IFN-gamma ELIspot with splenocytes or separated CD8+ or CD4+ cells from HLA-A*0201 tg mice vaccinated with Ipep1604+IC31.

Fig.10 shows mouse IFN-gamma ELIspot with splenocytes or separated CD8+ or CD4+ cells from HLA-B*0702tg mice vaccinated with Ipep1604+IC31.

E x a m p l e s :

General description of the examples:

The present examples show the performance of the present invention on a specific pathogen hepatitis C virus (HCV).

In the first part the method according to the present invention was applied, which is based on the use of "empty HLA molecules". These molecules were incubated with mixtures of potential HCV derived peptide ligands, screening for specific binding events. The possibility to use highly complex mixtures allows a very quick identification of the few binders out of hundreds or even thousands of potential ligands. This is demonstrated by using HLA-DRB1*0101, -DRB1*0401, -DRB1*0404, -DRB1*0701 molecules and pools of overlapping 15- to 23mers. Importantly, this analysis using multiple different HLA-alleles allows identifying promiscuous ligands capable to binding to more than one HLA allele. Promiscuous T-cell epitopes are particularly valuable components of epitope-based vaccines. They enable treating a higher portion of a population than epitopes restricted to one HLA allele.

The same process can be applied for class I molecules and peptides of appropriate length i.e. 8 to 11-mers. The ligand-pools can be synthetic overlapping peptides. Another possibility is to digest the antigen in question enzymatically or non-enzymatically. The latter achieved by alkali-hydrolysis generates all po-

tential degradation products and has been successfully used to identify T cell epitopes (Gavin 1993). Enzymatic digestions can be done with proteases. One rational way would further be to use proteases involved in the natural antigen-processing pathway like the proteasome for class I restricted epitopes (Heemels 1995) or cathepsins for class II restricted epitopes (Villadangos 2000). Ligand pools could also be composed of naturally occurring ligands obtained for instance by lysis of or elution from cells carrying the respective epitope. In this regard it is important to note that also non-peptide ligands like for instance glycolipids can be applied. It is known that non-classical class I molecules, which can be encoded by the MHC (e.g. HLA-G, HLA-E, MICA, MICB) or outside the MHC (e.g. CD1 family) can present various non-peptide ligands to lymphocytes (Kronenberg 1999). Use of recombinant "empty" nonclassical class I molecules would allow binding reactions and identification of binders in similar manner as described here.

After rapid identification of ligands capable of binding to HLA molecules the process according to the present invention also offers ways to characterize directly specific T cell responses against these binders. One possibility is to directly use the isolated HLA:ligand complex in a so called "synthetic T cell assay". The latter involves antigen-specific re-stimulation of T cells by the HLA:ligand complex together with a second signal providing co-stimulation like activation of CD28 by an activating antibody. This assay can be done in an ELIspot readout.

Another possibility is the immunization of HLA-transgenic mice to prove immunogenicity of ligands identified by the Epitope Capture approach as demonstrated in Example II.

MATERIALS & METHODS

Peptides

In order to identify conserved regions between HCV genotypes 1, 2 and 3, about 90 full genomes publicly available through Genebank were aligned. In total, 43% of the coding region of HCV was found to be conserved in at least 80% of clinical isolates. In

cases, where at a certain position consistently two distinct amino acids (eg. arginine or lysine) were found, both variants were considered for analysis. Altogether 148 conserved regions, longer than 8 amino acids were identified. Conserved region were spanned by ~500 fifteen amino acid residue (15mer) peptides, each peptide overlapping its precursor by 14 out of 15 amino acids. Conserved regions between 8 and 14 amino acids long were covered by further 80 (non-overlapping) 15mers. 15mers were synthesized using standard F-moc chemistry in parallel (288 at a time) on a Syro II synthesizer (Multisyntech, Witten, Germany). Each fourth 15mer was checked by mass spectrometry. 15mers were applied for experiments without further purification. In addition 63 peptides of 16-xx aa were synthesized using standard F-moc chemistry on an ABI 433A synthesizer (Applied Biosystems, Weiterstadt, Germany) and purified by RP-HPLC (Biocut 700E, Applied Biosystems, Langen, Germany) using a C18 column (either ODS ACU from YMC or 218TP, Vydac). Purity and identity were characterized by MALDI-TOF on a Reflex III mass-spectrometer (Bruker, Bremen, Germany). Peptides were solubilized in 100 % DMSO at ~10 mg/ml (~5 mM). Stocks of peptide pools (20 peptides each) were made in 100 % DMSO at a final concentration of 0.5 mg/ml (~0.25 mM) for each peptide. All peptides used in the present invention are listed in Table 1. Peptides YAR (YARFQSQTTLKQKT), HA (PKYVKQNTLKLAT), P1 (GYKVLVLNPSVAAT), P2 (HMWNFISGIQYLAGLSTLPGNPA), P3 (KFPGGGQIVGVYLLPRRRGPRL), P4 (DLMGYIPAV) and CLIP (KLPKPPKPVSKMRMATPLLMQALPM) were used as control peptides in binding assays.

Epitope capture and peptide binding assay

Soluble HLA class II DRA1*0101/DRB1*0101/Ii, DRA1*0101/DRB1*0401/Ii, DRA1*0101/DRB1*0404/Ii and DRA1*0101/DRB1*0701/Ii molecules were expressed in SC-2 cells and purified as described in Aichinger et al., 1997. In peptide binding reactions soluble DRB1*0101, DRB1*0401, DRB1*0404 molecules were used in a concentration of ~0.5 µM, and each single peptide was added in 10-fold molar excess (5 µM) if not mentioned differently. The concentration of DMSO in the binding reaction did not exceed 4 %. The reaction was performed in PBS buffer (pH 7.4) at room temperature for 48 hours in the presence

of a protease inhibitor cocktail (Roche) and 0.1 % octyl-beta-D-glucopyranoside (Sigma). Peptide binding was evaluated in an SDS-stability assay (Gorga et al., 1987): trimeric HLA class II alpha:beta:peptide complexes are resistant to SDS and consequently appear as ~60 kDa band in SDS-PAGE Western blot analysis. Individual HLA class II alpha- and beta-chains not stabilized by bound peptide migrate as ~35 kDa and ~25 kDa bands, respectively. Briefly, HLA-peptide complexes were treated with 1 % SDS at room temperature and resolved by SDS-PAGE run with 20 mA for approximately 2.5 hours at room temperature. Protein was transferred onto PVDF membrane by electroblotting, and stained with anti-alpha-chain TAL.1B5 or/and beta-chain MEM136 antibodies. For detection of Western-blot signals ECL solutions (Amersham) were used. For DRB1*0101 molecules HA and P1 peptides were used as controls for evaluation of strong binding, P2 peptide for intermediate binding and YAR as a negative control. For DRB1*0401 the strongest binding controls were YAR and HA peptides, while P1 and P2 served as an intermediate and weak binder, respectively. In the case of DRB1*0404 molecules P1 and P2 peptides were used to estimate strong binding, YAR peptide to control intermediate binding and HA peptide as an negative control. The binding affinities to DRB1*0701 were test by a peptide-competition assay (Reay et al., 1992). Briefly, binding of the biotinylated CLIP peptide with high affinity (reference peptide) has been used for monitoring of HLA:peptide complex formation. A testing peptide added to the binding reaction at an equimolar concentration to CLIP peptide could compete out CLIP when its affinity is higher or inhibit binding for 50 % if its affinity is equal to affinity of CLIP. In the case of lower affinity peptides they should be added in excess to the reference peptide to compete for occupancy of HLA binding grove. The values of the concentration of competitor peptides required for 50 % inhibition of reference peptide (biotinylated CLIP) binding (IC_{50}) can be used for evaluation of peptide binding affinities. Alternatively, comparing of the amount of reference peptide bound to HLA molecules in the presence or absence of competitor peptide one can determine the binding activity of the peptide of interest. In the present peptide-competition assay conditions of peptide binding were similar to described above. DRB1*0701 molecules were used in a concentration of ~0.5 μM and biotinylated

CLIP was added to all samples in the final concentration of 2 µM. Competitor peptides were added in three different concentrations: 2 nM, 20 µM and 200 µM. Binding reaction was performed in PBS buffer (pH 7.4) for 18 hours at 37°C. The amount of biotinylated CLIP associated with soluble DRB1*0701 molecules was determined by ELISA. Briefly, MaxiSorp 96-well plates (Nunc, Denmark) were coated with mouse anti-DR antibody L243 by overnight incubation with 50 µl of 10 µg/ml dilution in PBS at 4°C. Non-specific binding to wells awas blocked by incubation with T-PBS containing 3 % of BSA for 2 hours at 37°C and binding reactions were then "captured" for 2 hours at room temperature. Following extensive washing, HLA-assosiated peptide complexes were detected using alkaline phosphatase-streptavidin (Dako) and Sigma 104 phosphatase substrate. A microplate reader (VICTOR) was used to monitor optical density at 405 nm. Non-biotinylated CLIP, P1 and P2 peptides were used as positive controls to evaluate strong binding. Peptide P3 and P4 served as a weakly binding and non-binding control, respectively.

Immunization of HLA-transgenic mice

Immunogenicity of synthetic HCV-derived peptides was tested in HLA-DRB1*0401- and HLA-A*0201-transgenic mice as follows: Groups of 3 mice (female, 8 weeks of age) were injected subcutaneously into the flank (in total 100µg of peptide + 30µg oligodinucleotide CpI (Purimex, Göttingen, Germany) per mouse). One week after the vaccination, spleens were removed and the splenocytes were activated ex vivo with the peptide used for vaccination and an irrelevant negative control peptide to determine IFN-gamma-producing specific cells (mouse ELISpot assay).

Mouse splenocyte ELIspot assay for single cell IFN-gamma release ELISpot plates (MAHA S4510, Millipore, Germany) were rinsed with PBS (200 µl/well), coated with anti-mouse IFN-gamma mAb (clone R46A2; 100 µl/well of 5 µg/ml in 0.1 M $NaHCO_3$, pH 9.2-9.5) and incubated overnight at 4°C. Plates were washed four times with PBS/0.1% Tween 20 and incubated with PBS/1% BSA (200 µl/well) at room temperature for 2 h to block nonspecific binding. Spleen cells from vaccinated mice were prepared and plated at 1 x 10^6 - 3 x 10^5 cells/well and incubated overnight at 37°C/5% CO_2 either

in the presence of the immunizing antigen (peptide), control peptides or with medium alone. Subsequently, plates were washed four times and incubated with biotinylated anti-mouse IFN-gamma mAb (clone AN18.17.24, 100 µl/well of 2 µg/ml in PBS/1% BSA) for 2 h at 37°C. After washing, streptavidin-peroxidase (Roche Diagnostics, Vienna, Austria) was added (1/5000 in PBS, 100 µl/well) and plates were incubated at room temperature for 2 additional hours. Subsequently, substrate was added to the washed plates (100 µl/well of a mixture of 10 ml 100 mM Tris pH 7.5 supplemented with 200 µl of 40 mg/ml DAB stock containing 50 µl of 80 mg/ml $NiCl_2$ stock and 5 µl of 30% H_2O_2). The reaction was stopped after 20-30 minutes by washing the plates with tap water. Dried plates were evaluated with an ELISpot reader (BIOREADER 2000, BioSys, Karben, Germany).

IFN-gamma ELIspot with human PBMC

PBMC from HCV RNA-negativ therapy responders or subjects spontaneously recovered were collected and HLA-typed serologically. Whole blood was collected in ACD Vacutainer tubes (Becton Dickinson Europe, Erembodegem, Germany). PBMC were isolated on Lymphoprep (Nycomed Pharma AS, Oslo, Norway) using Leuco-sep tubes (Greiner, Frickenhausen, Germany), washed 3x with PBS (Invitrogen Life Technologies (formerly GIBCOBRL), Carlsbad, CA, USA) and resuspended at a concentration of $2x10^7$/ml in freezing medium consisting of 4 parts RPMI 1640 supplemented with 1 mM sodium pyruvate, 2 mM L-glutamine, 0.1 mM non-essential amino acids, 50 µM 2-mercaptoethanol (all from Invitrogen Life Technologies), 9 parts foetal bovine serum (FCS; from PAA, Linz, Austria) and 1 part DMSO (SIGMA, Deisenhofen, Germany). PBMC were stored over night in 1°C freezing containers (Nalgene Nunc International, Rochester, New York, USA) at -80°C and then transferred into liquid nitrogen. The ELIspot assay was essentially done as described (Lalvani et al.). Briefly, Multi Screen 96-well filtration plates MAIP S4510 (Millipore, Bedford, MA) were coated with 10 µg/ml (0,75 µg/well) anti-human IFN-g monoclonal antibody (Mab) B140 (Bender Med Systems, Vienna, Austria) over night at 4°C. Plates were washed 2 times with PBS (Invitrogen Life Technologies) and blocked with ELIspot medium (RPMI 1640 supplemented with 1 mM sodium pyruvate, 2 mM L-glutamine, 0.1 mM non-essential amino acids, 50 µM 2-mercaptoethanol (all from In-

vitrogen Life Technologies) and 10% human serum type AB (PAA, Linz, Austria). Cryo-preserved PBMC were thawed quickly in a 37°C water bath, washed 1x with ELISPOT medium and incubated overnight (37°C, 5% CO_2). The next day cells were plated at 200,000 PBMC/well and co-cultivated with either individual peptides (10 µg/ml) or peptide pools (each peptide at a final concentration of 5 µg/ml) for 20 hrs. After removing cells and washing 6 times with wash buffer (PBS; 0,1% Tween 20 from SIGMA), 100 µl of a 1:10000 dilution (0.015 µg/well) of the biotinylated anti-human IFN-γ MAb B308-BT2 (Bender Med Systems), was added for an incubation of 2 hrs at 37°C or alternatively for over night at 4°C. After washing, Streptavidin-alkaline phosphatase (DAKO, Glostrup, Denmark) was added at 1.2 µg/ml for 1 hr at 37°C. The assay was developed by addition of 100 µl/well BCIP/NBT alkaline phosphatase substrate (SIGMA).

In vitro priming of human PBMCs

Human PBMCs are repeatedly stimulated with antigen (peptide or peptide mixture) in the presence of IL-2 and IL-7. This leads to the selective oligoclonal expansion of antigen-specific T cells. Responses against individual epitopes can be assessed for instance by IFN-γ ELIspot assays.Freshly thawed PBMCs were cultured in 6 well plates (2-4x 10^6/mL viable cells) in RPMI-1640 (GibcoBRL), 1% non-essential amino acids (GibcoBRL, cat# 11140-035), 1% Penicillin (10,000 U/ml)-Streptomycin (10,000 µg/ml) (GibcoBRL, cat#15140-122), 1% L-Glutamine (GibcoBRL), 0.1% beta-mercapto-ethanol (GibcoBRL), 1% Na-pyruvate (GibcoBRL), plus 10% Human AB serum (PAA, Linz, Austria). Peptides (10µM each) were added to each well. rhIL-7 (Strathmann Biotech) was added at 10 ng/mL final concentration. 20-30 U/mL rhIL-2 (Strathmann Biotech) were added on day 4. On day 10, all cells were removed from plates, washed once in media (as above), and counted. For the next cycle of in vitro priming, viable cells were co-cultivated with autologous gamma irradiated (1.2 gray/min, for 20 minutes) PBMC as feeders (plated at 100,000 per well) and peptides, rh-IL-2 as described above. ELIspot was done as described above, except that 200,000 responder cells (pre-stimulated for 2 rounds of in vitro priming) were used together with 60,000 autologous irradiated responder cells.

Example I. Rapid identification of promiscuous HLA-binding peptides from HCV by measuring peptide pools arrayed in matrix format

To span conserved regions within the HCV polyprotein more than 640 peptides were synthesized (Table 1). For rapid identification of HLA ligands and novel T-cell epitopes, 40 peptide pools each containing 20 single peptides were prepared. The pools were constructed in a way that each peptide was present in 2 pools (matrix format). This allows identification of reactive peptides at the crossover points of row- and column mixtures (Fig. 1 HCV peptide matrix).

Table 1. Synthetic peptides derived from conserved regions of HCV.

Peptide ID		Peptide ID		Peptide ID		Peptide ID	
A	1	MSTNPKPQRKTKRNTR	73	RHRSRNVGKVIDTLTC	145	CTVNYTIFKIRMVYGG	A 217	ADGGCSGGAYDIIIC
A	2	STNPKPQRKTKRNTRN	80	RSRNVGKVIDTLTCGF	146	TVNYTIFKIRMVYGG	A [illegible]	DGGCSGGAYDIIICD
A	3	TNPKPQRKTKRNTRNR	81	SRNVGKVIDTLTCGFA	147	VNYTIFKIRMVYGGV	A 219	GGCSGGAYDIIICDE
A	4	NPKPQRKTKRNTRNRP	82	RNVGKVIDTLTCGFAD	148	NYTIFKIRMVYGGVE	A 220	GCSGGAYDIIICDEC
A	5	PKPQRKTKRNTRNRPQ	83	NVGKVIDTLTCGFADL	149	YTIFKIRMVYGGVEH	A 221	CSGGAYDIIICDECH
A	6	KPQRKTKRNTRNRPQD	84	VGKVIDTLTCGFADL	150	TIFKIRMVYGGVEHR	A 222	SGGAYDIIICDECHS
A	7	PQRKTKRNTRNRPQD	85	TLTCGFADLMGYIPV	151	IFKIRMVYGGVEHRL	A 223	TTILGIGTVLDQAET
A	8	QRKTKRNTRNRPQDV	86	LTCGFADLMGYIPVV	152	FKIRMVYGGVEHRLN	A 224	TILGIGTVLDQAETA
A	9	RKTKRNTRNRPQDVK	87	TCGFADLMGYIPVVG	153	PALSTGLLHLHQNIV	A 225	ILGIGTVLDQAETAG
A	10	KTKRNTRNRPQDVKF	88	CGFADLMGYIPVVGA	154	ALSTGLLHLHQNIVD	A 226	LGIGTVLDQAETAGA
A	11	TKRNTRNRPQDVKFP	89	GFADLMGYIPVVGAP	155	LSTGLLHLHQNIVDV	A 227	GIGTVLDQAETAGAR
A	12	KRNTRNRPQDVKFPG	90	FADLMGYIPVVGAPL	156	STGLLHLHQNIVDVQ	A 228	IGTVLDQAETAGARL
A	13	RNTRNRPQDVKFPGG	91	ADLMGYIPVVGAPLG	157	TGLLHLHQNIVDVQY	A 229	GTVLDQAETAGARLV
A	14	NTRNRPQDVKFPGGG	92	DLMGYIPVVGAPLGG	158	GLLHLHQNIVDVQYL	A 230	TVLDQAETAGARLVV
A	15	TRNRPQDVKFPGGGQ	93	LMGYIPVVGAPLGGV	159	LLHLHQNIVDVQYLY	A 231	VLDQAETAGARLVVL
A	16	RNRPQDVKFPGGGQI	94	MGYIPVVGAPLGGVA	160	LHLHQNIVDVQYLYG	A 232	LDQAETAGARLVVLA
A	17	NRPQDVKFPGGGQIV	95	GYIPVVGAPLGGVAR	161	HLHQNIVDVQYLYGI	A 233	DQAETAGARLVVLAT
A	18	RPQDVKFPGGGQIVG	96	YIPVVGAPLGGVARA	162	LHQNIVDVQYLYGIG	A 234	QAETAGARLVVLATA
A	19	PQDVKFPGGGQIVGG	97	IPVVGAPLGGVARAL	163	HQNIVDVQYLYGIGS	A 235	AETAGARLVVLATAT
A	20	QDVKFPGGGQIVGGV	98	PVVGAPLGGVARALA	164	QNIVDVQYLYGIGSA	A 236	ETAGARLVVLATATP
A	21	DVKFPGGGQIVGGVY	99	VVGAPLGGVARALAH	165	NIVDVQYLYGIGSAV	A 237	TAGARLVVLATATPP
A	22	VKFPGGGQIVGGVYL	100	VGAPLGGVARALAHG	166	IVDVQYLYGIGSAVK	A 238	AGARLVVLATATPPG
A	23	KFPGGGQIVGGVYLL	101	GAPLGGVARALAHGV	167	VDVQYLYGIGSAVKS	A 239	GARLVVLATATPPGS
A	24	FPGGGQIVGGVYLLP	102	APLGGVARALAHGVR	168	DVQYLYGIGSAVKSG	A 240	ARLVVLATATPPGSV
A	25	PGGGQIVGGVYLLPR	103	PLGGVARALAHGVRV	169	VQYLYGIGSAVKSGV	A 241	RLVVLATATPPGSVT
A	26	GGGQIVGGVYLLPRR	104	LGGVARALAHGVRVL	170	QYLYGIGSAVKSGVA	A 242	LVVLATATPPGSVTV
A	27	GGQIVGGVYLLPRRG	105	GGVARALAHGVRVLE	171	YLYGIGSAVKSGVAK	A 243	VVLATATPPGSVTVP
A	28	GQIVGGVYLLPRRGR	106	GVARALAHGVRVLED	172	LYGIGSAVKSGVAKH	A 244	VLATATPPGSVTVPH
A	29	QIVGGVYLLPRRGRH	107	VARALAHGVRVLEDG	173	YGIGSAVKSGVAKHV	A 245	LATATPPGSVTVPHP
A	30	IVGGVYLLPRRGRHI	108	ARALAHGVRVLEDGV	174	GIGSAVKSGVAKHVV	A 246	ATATPPGSVTVPHPN
A	31	VGGVYLLPRRGRHIG	109	RALAHGVRVLEDGVN	175	IGSAVKSGVAKHVVD	A 247	TATPPGSVTVPHPNI
A	32	GGVYLLPRRGRHIGV	110	ALAHGVRVLEDGVNY	176	GSAVKSGVAKHVVDL	A 248	ATPPGSVTVPHPNIE
A	33	GVYLLPRRGRHIGVE	111	LAHGVRVLEDGVNYA	177	SAVKSGVAKHVVDLM	A 249	TPPGSVTVPHPNIEE
A	34	VYLLPRRGRHIGVEE	112	AHGVRVLEDGVNYAT	178	AVKSGVAKHVVDLMC	A 250	PPGSVTVPHPNIEEV
A	35	YLLPRRGRHIGVRAT	113	HGVRVLEDGVNYATG	179	VKSGVAKHVVDLMCH	A 251	PGSVTVPHPNIEEVA
A	36	LLPRRGRHIGVRATR	114	GVRVLEDGVNYATGN	180	KSGVAKHVVDLMCHA	A 252	GSVTVPHPNIEEVAL
A	37	LPRRGRHIGVRATRK	115	VRVLEDGVNYATGNL	181	SGVAKHVVDLMCHAT	A 253	SVTVPHPNIEEVALS
A	38	PRRGRHIGVRATRKS	116	RVLEDGVNYATGNLP	182	GVAKHVVDLMCHATF	A 254	VTVPHPNIEEVALST
A	39	RRGRHIGVRATRKTS	117	VLEDGVNYATGNLPG	183	VAKHVVDLMCHATFT	A 255	TVPHPNIEEVALSTT
A	40	RGRHIGVRATRKTSE	118	LEDGVNYATGNLPGC	184	AKHVVDLMCHATFTS	A 256	VPHPNIEEVALSTTG
A	41	GRHIGVRATRKTSER	119	EDGVNYATGNLPGCS	185	KHVVDLMCHATFTSR	A 257	PHPNIEEVALSTTGE
A	42	RHIGVRATRKTSERS	120	DGVNYATGNLPGCSF	186	HVVDLMCHATFTSRC	A 258	HPNIEEVALSTTGEI
A	43	HIGVRATRKTSERSQ	121	GVNYATGNLPGCSFS	187	VVDLMCHATFTSRCL	A 259	PNIEEVALSTTGEIP
A	44	IGVRATRKTSERSQP	122	VNYATGNLPGCSFSI	188	VDLMCHATFTSRCLA	A 260	NIEEVALSTTGEIPF
A	45	GVRATRKTSERSQPR	123	NYATGNLPGCSFSIF	189	DLMCHATFTSRCLAV	A 261	IEEVALSTTGEIPFY
A	46	VRATRKTSERSQPRG	124	YATGNLPGCSFSIFL	190	LMCHATFTSRCLAVN	A 262	EEVALSTTGEIPFYG
A	47	RATRKTSERSQPRGR	125	ATGNLPGCSFSIFLL	191	MCHATFTSRCLAVNQ	A 263	EVALSTTGEIPFYGK
A	48	ATRKTSERSQPRGRR	126	TGNLPGCSFSIFLLA	192	CHATFTSRCLAVNQE	A 264	VALSTTGEIPFYGKA
A	49	TRKTSERSQPRGRRQ	127	GNLPGCSFSIFLLAL	193	HATFTSRCLAVNQEP	A 265	ALSTTGEIPFYGKAI
A	50	RKTSERSQPRGRRQP	128	NLPGCSFSIFLLALS	194	ATFTSRCLAVNQEPG	A 266	LSTTGEIPFYGKAIP
A	51	KTSERSQPRGRRQPI	129	LPGCSFSIFLLALSC	195	TFTSRCLAVNQEPGV	A 267	STTGEIPFYGKAIPL
A	52	TSERSQPRGRRQPIP	130	PGCSFSIFLLALSCL	196	FTSRCLAVNQEPGVL	A 268	TTGEIPFYGKAIPLE
A	53	SERSQPRGRRQPIPK	131	GCSFSIFLLALSCLT	197	TSRCLAVNQEPGVLV	A 269	TGEIPFYGKAIPLEV
A	54	ERSQPRGRRQPIPKA	132	CSFSIFLLALSCLTV	198	SRCLAVNQEPGVLVK	A 270	GEIPFYGKAIPLEVI
A	55	RSQPRGRRQPIPKAR	133	SFSIFLLALSCLTVP	199	RCLAVNQEPGVLVKT	A 271	EIPFYGKAIPLEVIK
A	56	SQPRGRRQPIPKARR	134	FSIFLLALSCLTVPA	200	CLAVNQEPGVLVKTL	A 272	IPFYGKAIPLEVIKG
A	57	QPRGRRQPIPKARRP	135	SIFLLALSCLTVPAS	201	LAVNQEPGVLVKTLT	A 273	PFYGKAIPLEVIKGG
A	58	PRGRRQPIPKARRPE	136	IFLLALSCLTVPASA	202	AVNQEPGVLVKTLTG	A 274	FYGKAIPLEVIKGGR
A	59	RGRRQPIPKARRPEG	137	FLLALSCLTVPASAY	203	VNQEPGVLVKTLTGG	A 275	YGKAIPLEVIKGGRH
A	60	GRRQPIPKARRPEGR	138	LLALSCLTVPASAYQ	204	NQEPGVLVKTLTGGR	B 5	SGMFDSSVLCECYDA
A	61	RRQPIPKARRPEGRT	139	LALSCLTVPASAYQV	205	QEPGVLVKTLTGGRN	B 6	GMFDSSVLCECYDAG
A	62	RQPIPKARRPEGRTW	140	ALSCLTVPASAYQVR	206	EPGVLVKTLTGGRNL	B 7	MFDSSVLCECYDAGC
A	63	QPIPKARRPEGRTWA	141	LSCLTVPASAYQVRN	207	PGVLVKTLTGGRNLV	B 8	FDSSVLCECYDAGCA
A	64	PIPKARRPEGRTWAQ	142	SCLTVPASAYQVRNS	208	GVLVKTLTGGRNLVF	B 9	DSSVLCECYDAGCAW
A	65	IPKARRPEGRTWAQP	143	CLTVPASAYQVRNSS	209	VLVKTLTGGRNLVFC	B 10	SSVLCECYDAGCAWY
A	66	PKARRPEGRTWAQPG	144	LTVPASAYQVRNSSG	210	LVKTLTGGRNLVFCT	B 11	SVLCECYDAGCAWYE
A	67	KARRPEGRTWAQPGY	145	TVPASAYQVRNSSGL	211	VKTLTGGRNLVFCTS	B 12	VLCECYDAGCAWYEL
A	68	ARRPEGRTWAQPGYP	146	VPASAYQVRNSSGLY	212	KTLTGGRNLVFCTSV	B 13	LCECYDAGCAWYELT
A	69	RRPEGRTWAQPGYPW	147	PASAYQVRNSSGLYH	213	TLTGGKSTKVPAYAA	B 14	CECYDAGCAWYELTP
A	70	RPEGRTWAQPGYPWP	148	ASAYQVRNSSGLYHV	214	LTGGKSTKVPAYAAQ	B 15	ECYDAGCAWYELTPA
A	71	PEGRTWAQPGYPWPL	149	SAYQVRNSSGLYHVT	215	TGGKSTKVPAYAAQG	B 16	CYDAGCAWYELTPAE
A	72	EGRTWAQPGYPWPLY	150	AYQVRNSSGLYHVTN	216	GGKSTKVPAYAAQGY	B 17	YDAGCAWYELTPAET
A	73	GRTWAQPGYPWPLYG	151	YQVRNSSGLYHVTND	217	GKSTKVPAYAAQGYK	B 18	DAGCAWYELTPAETT
A	74	RTWAQPGYPWPLYGN	152	QVRNSSGLYHVTNDC	218	KSTKVPAYAAQGYKV	B 19	AGCAWYELTPAETTV
A	75	TWAQPGYPWPLYGNE	153	VRNSSGLYHVTNDCS	219	STKVPAYAAQGYKVL	B 20	GCAWYELTPAETTVR
A	76	WAQPGYPWPLYGNEG	154	RNSSGLYHVTNDCSN	220	TKVPAYAAQGYKVLV	B 21	CAWYELTPAETTVRL
A	77	AQPGYPWPLYGNEGL	155	NSSGLYHVTNDCSNS	221	KVPAYAAQGYKVLVL	B 22	AWYELTPAETTVRLR
A	78	QPGYPWPLYGNEGLG	156	SSGLYHVTNDCSNSI	222	VPAYAAQGYKVLVLN	B 23	WYELTPAETTVRLRA
A	79	PGYPWPLYGNEGLGW	157	SGLYHVTNDCSNSIV	223	PAYAAQGYKVLVLNP	B 24	YELTPAETTVRLRAY
A	80	GYPWPLYGNEGLGWA	158	GLYHVTNDCSNSIVY	224	AYAAQGYKVLVLNPS	B 25	ELTPAETTVRLRAYM
A	81	YPWPLYGNEGLGWAG	159	LYHVTNDCSNSIVYE	225	YAAQGYKVLVLNPSV	B 26	LTPAETTVRLRAYMN
A	82	PWPLYGNEGLGWAGW	160	YHVTNDCSNSIVYEA	226	AAQGYKVLVLNPSVA	B 27	TPAETTVRLRAYMNT
A	83	WPLYGNEGLGWAGWL	161	HVTNDCSNSIVYEAA	227	AQGYKVLVLNPSVAA	B 28	PAETTVRLRAYMNTP
A	84	PLYGNEGLGWAGWLL	162	VTNDCSNSIVYEAAD	228	QGYKVLVLNPSVAAT	B 29	AETTVRLRAYMNTPG
A	85	LYGNEGLGWAGWLLS	163	TNDCSNSIVYEAADM	229	GYKVLVLNPSVAATL	B 30	ETTVRLRAYMNTPGL
A	86	YGNEGLGWAGWLLSP	164	NDCSNSIVYEAADMI	230	YKVLVLNPSVAATLG	B 31	TTVRLRAYMNTPGLP
A	87	GNEGLGWAGWLLSPR	165	DCSNSIVYEAADMIM	231	KVLVLNPSVAATLGF	B 32	TVRLRAYMNTPGLPV
A	88	NEGLGWAGWLLSPRG	166	CSNSIVYEAADMIMH	232	VLVLNPSVAATLGFG	B 33	VRLRAYMNTPGLPVC
A	89	EGLGWAGWLLSPRGS	167	SNSIVYEAADMIMHT	233	LVLNPSVAATLGFGA	B 34	RLRAYMNTPGLPVCQ
A	90	GLGWAGWLLSPRGSR	168	NSIVYEAADMIMHTP	234	VLNPSVAATLGFGAY	B 35	LRAYMNTPGLPVCQD
A	91	LGWAGWLLSPRGSRP	169	SIVYEAADMIMHTPP	235	LNPSVAATLGFGAYM	B 36	RAYMNTPGLPVCQDH
A	92	GWAGWLLSPRGSRPS	170	IVYEAADMIMHTPPG	236	NPSVAATLGFGAYMS	B 37	AYMNTPGLPVCQDHL
A	93	WAGWLLSPRGSRPSW	171	VYEAADMIMHTPPGI	237	PSVAATLGFGAYMSK	B 38	YMNTPGLPVCQDHLE
A	94	AGWLLSPRGSRPSWG	172	YEAADMIMHTPPGIV	238	SVAATLGFGAYMSKA	B 39	MNTPGLPVCQDHLEF
A	95	GWLLSPRGSRPSWGP	173	EAADMIMHTPPGIVG	239	VAATLGFGAYMSKAH	B 40	NTPGLPVCQDHLEFL
A	96	WLLSPRGSRPSWGPT	174	AADMIMHTPPGIVGG	240	AATLGFGAYMSKAHG	B 41	TPGLPVCQDHLEFLE
A	97	LLSPRGSRPSWGPTD	175	ADMIMHTPPGIVGGV	241	ATLGFGAYMSKAHGI	B 42	PGLPVCQDHLEFLEE
A	98	LSPRGSRPSWGPTDP	176	DMIMHTPPGIVGGVL	242	TLGFGAYMSKAHGID	B 43	GLPVCQDHLEFLEES
A	99	SPRGSRPSWGPTDPR	177	MIMHTPPGIVGGVLR	243	LGFGAYMSKAHGIDP	B 44	LPVCQDHLEFLEESL
A	100	PRGSRPSWGPTDPRH	178	IMHTPPGIVGGVLRA	244	GFGAYMSKAHGIDPN	B 45	PVCQDHLEFLEESLT
A	101	RGSRPSWGPTDPRHR	179	MHTPPGIVGGVLRAL	245	FGAYMSKAHGIDPNI	B 46	VCQDHLEFLEESLTG
A	102	GSRPSWGPTDPRHRS	180	HTPPGIVGGVLRALT	246	GAYMSKAHGIDPNIR	B 47	CQDHLEFLEESLTGI
A	103	SRPSWGPTDPRHRSR	181	TPPGIVGGVLRALTA	247	AYMSKAHGIDPNIRT	B 48	QDHLEFLEESLTGIH
A	104	RPSWGPTDPRHRSRN	182	PPGIVGGVLRALTAY	248	YMSKAHGIDPNIRTG	B 49	DHLEFLEESLTGIHE
A	105	PSWGPTDPRHRSRNV	183	PGIVGGVLRALTAYS	249	MSKAHGIDPNIRTGV	B 50	HLEFLEESLTGIHEV
A	106	SWGPTDPRHRSRNVG	184	GIVGGVLRALTAYSQ	250	SKAHGIDPNIRTGVR	B 51	LEFLEESLTGIHEVM
A	107	WGPTDPRHRSRNVGK	185	IVGGVLRALTAYSQQ	251	KAHGIDPNIRTGVRT	B 52	EFLEESLTGIHEVMN
A	108	GPTDPRHRSRNVGKV	186	VGGVLRALTAYSQQK	252	AHGIDPNIRTGVRTI	B 53	FLEESLTGIHEVMNL
A	109	PTDPRHRSRNVGKVI	187	GGVLRALTAYSQQKK	253	HGIDPNIRTGVRTIT	B 54	LEESLTGIHEVMNLE
A	110	TDPRHRSRNVGKVID	188	GVLRALTAYSQQKKG	254	GIDPNIRTGVRTITT	B 55	EESLTGIHEVMNLEQ
A	111	DPRHRSRNVGKVIDT	189	VLRALTAYSQQKKGL	255	IDPNIRTGVRTITTG	B 56	ESLTGIHEVMNLEQR
A	112	PRHRSRNVGKVIDTL	190	LRALTAYSQQKKGLI	256	DPNIRTGVRTITTGA	B 57	SLTGIHEVMNLEQRN
A	113	RHRSRNVGKVIDTLT	191	RALTAYSQQKKGLIF	257	PNIRTGVRTITTGAP	B 58	LTGIHEVMNLEQRNL
A	114	HRSRNVGKVIDTLTC	192	ALTAYSQQKKGLIFG	258	NIRTGVRTITTGAPV	B 59	TGIHEVMNLEQRNLE
A	115	RSRNVGKVIDTLTCG	193	LTAYSQQKKGLIFGK	259	IRTGVRTITTGAPVT	B 60	GIHEVMNLEQRNLEL
A	116	SRNVGKVIDTLTCGF	194	TAYSQQKKGLIFGKG	260	RTGVRTITTGAPVTQ	B 61	IHEVMNLEQRNLELR
A	117	RNVGKVIDTLTCGFA	195	AYSQQKKGLIFGKGK	261	TGVRTITTGAPVTQS	B 62	HEVMNLEQRNLELRR
A	118	NVGKVIDTLTCGFAD	196	YSQQKKGLIFGKGKG	262	GVRTITTGAPVTQSM	B 63	EVMNLEQRNLELRRS
A	119	VGKVIDTLTCGFADL	197	SQQKKGLIFGKGKGA	263	VRTITTGAPVTQSMG	B 64	VMNLEQRNLELRRSC
A	120	GKVIDTLTCGFADLM	198	QQKKGLIFGKGKGAV	264	RTITTGAPVTQSMGL	B 65	MNLEQRNLELRRSCD
A	121	KVIDTLTCGFADLMG	199	QKKGLIFGKGKGAVE	265	TITTGAPVTQSMGLV	B 66	NLEQRNLELRRSCDL
A	122	VIDTLTCGFADLMGY	200	KKGLIFGKGKGAVEF	266	ITTGAPVTQSMGLVC	B 67	LEQRNLELRRSCDLA
A	123	IDTLTCGFADLMGYI	201	KGLIFGKGKGAVEFY	267	TTGAPVTQSMGLVCG	B 68	EQRNLELRRSCDLAT
A	124	DTLTCGFADLMGYIP	202	GLIFGKGKGAVEFYE	268	TGAPVTQSMGLVCGV	B 69	QRNLELRRSCDLATS
A	125	TLTCGFADLMGYIPV	203	LIFGKGKGAVEFYEF	269	GAPVTQSMGLVCGVY	B 70	RNLELRRSCDLATSV
A	126	LTCGFADLMGYIPVV	204	IFGKGKGAVEFYEFV	270	APVTQSMGLVCGVYY	B 71	NLELRRSCDLATSVT
A	127	TCGFADLMGYIPVVG	205	FGKGKGAVEFYEFVK	271	PVTQSMGLVCGVYYR	B 72	LELRRSCDLATSVTE
A	128	CGFADLMGYIPVVGA	206	GKGKGAVEFYEFVKL	272	VTQSMGLVCGVYYRL	B 73	ELRRSCDLATSVTEL
A	129	GFADLMGYIPVVGAP	207	KGKGAVEFYEFVKLH	273	TQSMGLVCGVYYRLG	B 74	LRRSCDLATSVTELT
A	130	FADLMGYIPVVGAPL	208	GKGAVEFYEFVKLHL	274	QSMGLVCGVYYRLGA	B 75	RRSCDLATSVTELTG
A	131	ADLMGYIPVVGAPLG	209	KGAVEFYEFVKLHLH	275	SMGLVCGVYYRLGAV	B 76	RSCDLATSVTELTGY
A	132	DLMGYIPVVGAPLGG	210	GAVEFYEFVKLHLHG	276	MGLVCGVYYRLGAVQ	B 77	SCDLATSVTELTGYM
A	133	LMGYIPVVGAPLGGV	211	AVEFYEFVKLHLHGP	277	GLVCGVYYRLGAVQN	B 78	CDLATSVTELTGYMP
A	134	MGYIPVVGAPLGGVA	212	VEFYEFVKLHLHGPT	278	LVCGVYYRLGAVQNE	B 79	DLATSVTELTGYMPT
A	135	GYIPVVGAPLGGVAR	213	EFYEFVKLHLHGPTP	279	VCGVYYRLGAVQNEV	B 80	LATSVTELTGYMPTF
A	136	YIPVVGAPLGGVARA	214	FYEFVKLHLHGPTPL	280	CGVYYRLGAVQNEVT	B 81	ATSVTELTGYMPTFM
A	137	IPVVGAPLGGVARAL	215	YEFVKLHLHGPTPLL	281	GVYYRLGAVQNEVTT	B 82	TSVTELTGYMPTFMC
A	138	PVVGAPLGGVARALA	216	EFVKLHLHGPTPLLY	282	VYYRLGAVQNEVTTS	B 83	SVTELTGYMPTFMCE
A	139	VVGAPLGGVARALAH	217	FVKLHLHGPTPLLYR	283	YYRLGAVQNEVTTSH	B 84	VTELTGYMPTFMCEH
A	140	VGAPLGGVARALAHG	218	VKLHLHGPTPLLYRL	284	YRLGAVQNEVTTSHP	B 85	TELTGYMPTFMCEHD
A	141	GAPLGGVARALAHGV	219	KLHLHGPTPLLYRLG	285	RLGAVQNEVTTSHPV	B 86	ELTGYMPTFMCEHDL
A	142	APLGGVARALAHGVR	220	LHLHGPTPLLYRLGA	286	LGAVQNEVTTSHPVT	B 87	LTGYMPTFMCEHDLT
A	143	PLGGVARALAHGVRV	221	HLHGPTPLLYRLGAV	287	GAVQNEVTTSHPVTR	B 88	TGYMPTFMCEHDLTV
A	144	LGGVARALAHGVRVL	222	LHGPTPLLYRLGAVQ	288	AVQNEVTTSHPVTRY	B 89	GYMPTFMCEHDLTVT
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B	94 ILAGSGAGVAGALVA
B	95 LAGSGAGVAGALVAF
B	96 AGSGAGVAGALVAFK
B	97 GSGAGVAGALVAFKK
B	98 SGAGVAGALVAFKKM
B	99 GAGVAGALVAFKKMS
B	100 AGVAGALVAFKKMSG
B	101 GVAGALVAFKKMSGE
B	102 VAGALVAFKKMSGEF
B	103 AGALVAFKKMSGEFM
B	104 GALVAFKKMSGEFMI
B	105 ALVAFKKMSGEFMIA
B	106 LVAFKKMSGEFMIAG
B	107 VAFKKMSGEFMIAGG
B	108 AFKKMSGEFMIAGGS
B	109 FKKMSGEFMIAGGSI
B	110 KKMSGEFMIAGGSIG
B	111 KMSGEFMIAGGSIGA
B	112 MSGEFMIAGGSIGAL
B	113 SGEFMIAGGSIGALV
B	114 GEFMIAGGSIGALVA
B	115 EFMIAGGSIGALVAF
B	116 FMIAGGSIGALVAFK
B	117 MIAGGSIGALVAFKM
B	118 IAGGSIGALVAFKMS
B	119 AGGSIGALVAFKMSG

Peptide ID	
B	120 AGSIGALVAFKMSG
B	121 GSGALVAFKMSGE
B	122 VNLLPAILSPGALVG
B	123 NLLPAILSPGALVVG
B	124 LLPAILSPGALVVGV
C	1 LPAILSPGALVVGVV
C	2 PAILSPGALVVGVVC
C	3 AILSPGALVVGVVCA
C	4 ILSPGALVVGVVCAA
C	5 LSPGALVVGVVCAAL
C	6 SPGALVVGVVCAALR
C	7 PGALVVGVVCAALRL
C	8 GALVVGVVCAALRRH
C	9 ALVVGVVCAALRRHV
C	10 LVVGVVCAALRRHVG
C	11 VVGVVCAALRRHVGP
C	12 VGVVCAALRRHVGPG
C	13 GVVCAALRRHVGPGG
C	14 VVCAALRRHVGPGES
C	15 VCAALRRHVGPGEGG
C	16 CAALRRHVGPGEGAV
C	17 AALRRHVGPGEGAVQ
C	18 ALRRHVGPGEGAVQW
C	19 LRRHVGPGEGAVQWM
C	20 RRHVGPGEGAVQWMN
C	21 RHVGPGEGAVQWMNR
C	22 HVGPGEGAVQWMNRL
C	23 VGPGEGAVQWMNRLI
C	24 GPGEGAVQWMNRLIA
C	25 GPGEGAVQWMNRLIA
C	26 PGEGAVQWMNRLIAF
C	27 GEGAVQWMNRLIAFA
C	28 EGAVQWMNRLIAFAS
C	29 GAVQWMNRLIAFASR
C	30 AVQWMNRLIAFASRG
C	31 VQWMNRLIAFASRGN
C	32 QWMNRLIAFASRGNH
C	33 WMNRLIAFASRGNHV
C	34 MNRLIAFASRGNHVS
C	35 NRLIAFASRGNHVSP
C	36 RLIAFASRGNHVSPT
C	37 LIAFASRGNHVSPTH
C	38 IAFASRGNHVSPTHV
C	39 AFASRGNHVSPTHVV
C	40 FASRGNHVSPTHVVL
C	41 ASRGNHVSPTHVVLP
C	42 SRGNHVSPTHVVLPG
C	43 RGNHVSPTHVVLPGL
C	44 GNHVSPTHVVLPGLV
C	45 NHVSPTHVVLPGLVG
C	46 HVSPTHVVLPGLVGV
C	47 VSPTHVVLPGLVGVC
C	48 SPTHVVLPGLVGVCA
C	49 PTHVVLPGLVGVCAA
C	50 THVVLPGLVGVCAAL
C	51 HVVLPGLVGVCAALR
C	52 VVLPGLVGVCAALRR
C	53 VLPGLVGVCAALRRH
C	54 LPGLVGVCAALRRHV
C	55 PGLVGVCAALRRHVG
C	56 GLVGVCAALRRHVGP
C	57 LVGVCAALRRHVGPG
C	58 VGVCAALRRHVGPGE
C	59 GVCAALRRHVGPGEG
C	60 VCAALRRHVGPGEGA
C	61 CAALRRHVGPGEGAV
C	62 AALRRHVGPGEGAVQ
C	63 ALRRHVGPGEGAVQW
C	64 LRRHVGPGEGAVQWM
C	65 RRHVGPGEGAVQWMN
C	66 RHVGPGEGAVQWMNR
C	67 HVGPGEGAVQWMNRL
C	68 VGPGEGAVQWMNRLI
C	69 GPGEGAVQWMNRLIA
C	70 PGEGAVQWMNRLIAF
C	71 GEGAVQWMNRLIAFA
C	72 EGAVQWMNRLIAFAS
C	73 VFDLGVRVCEKMALY
C	74 VFDLGVRVCEKMAL

Peptide ID	
C	75 FDLGVRVCEKMALY
C	76 DLGVRVCEKMALYDV
C	77 LGVRVCEKMALYDV
C	78 GVRVCEKMALYDVL
C	79 GGKKAARLIVYPDLG
C	80 GKKAARLIVYPDLGV
C	81 KKAARLIVYPDLGVR
C	82 KAARLIVYPDLGVRV
C	83 AARLIVYPDLGVRVC
C	84 ARLIVYPDLGVRVCE
C	85 RLIVYPDLGVRVCEK
C	86 LIVYPDLGVRVCEKM
C	87 IVYPDLGVRVCEKMA
C	88 VYPDLGVRVCEKMAL
C	89 YPDLGVRVCEKMALY
C	90 AQPGYPWPLYGNEGL
C	91 QPGYPWPLYGNEGLC
C	92 PGYPWPLYGNEGLCS
C	93 AFCSALYVGDLCGSV
C	94 ETVQDCNCSIYPGHV
C	95 EFVQDCNCSIYPGHV
C	96 GVLAGLAYYSMVGNW
C	97 GVLFGLAYFSMVGNW
C	98 DQRPYCWHYPRPCG
C	99 DQRPYCWHYPRPRCG
C	100 TGPTDCFRKHPEATY
C	101 YTKQSSGPWLTPRCL
C	102 LMAACNWTRGERCDL
C	103 LMAACNFTRGEPCDL
C	104 IAQAEAALENLVVLH
C	105 IAQAEAALEKLVVLH
C	106 TRVPYFVRAGLIRA
C	107 TRVPYFVRAHGLIRA
C	108 HAGLRDLAAVAEPVV
C	109 AAGLRDLAVAVEPIV
C	110 TWGADTAACGCIIL
C	111 TWSAETAACGCILL
C	112 GQGSWRLLAPITAYSQ
C	113 TAYSQGTRGLLGCIT
C	114 TAYSQGTRGLLGCIV
C	115 SCIITSLTGRDNKQV
C	116 GCIVVSMTGRDKTQV
C	117 VNGVCWTVYHGAGSK
C	118 KGPITGMYTNVDQDL
C	119 KGPITGMYSSAEQDL
C	120 GDSRGSLLSPRPVSY
C	121 GDSRGALLSPRPVSY
C	122 SYLKGSSGGPLCPS
C	123 SYLKGSSGGPVLCPS
C	124 GHAVGIFRAAVCTRG
C	125 GVDPWRTGVRTTITT
C	126 VPHPNIEEVALSNTS
C	127 TGEIPFYGKAIPIEV
C	128 TGEIPFYGKAIPLEV
C	129 PTSGDVVVATDALM
C	130 QTVDFSLDPTFTIET
C	131 TLHGPTPLLYRLGAV
C	132 VGNEVFILTPITNYI
C	133 LVRGFTDEMEECASHL
C	134 TTLLFNILGGWVAAQ
C	135 TTLLFNILGSWVAAQ
C	136 PSAASAFVGAGIAGA
C	137 PSAATGFVSGLAGA
C	138 TPCSGSWLRDVWDWI
C	139 VAAEEVVETVRQGF
C	140 VAAEEYAEVTRTGF
C	141 FFTEVDGVRLHRYAP
C	142 FFTELDGVRLHRYAP
C	143 FFTWVDGVQHIRYAP
C	144 FFTWLDGKVQHIRYAP
C	145 YLVGSQLPCEPEPDV
C	146 YLVGSQLPCDPEPDV
C	147 LPWAPDVINPPLLE
C	148 ASLRQKKVTFDRLGV
C	149 ASLRAKKVTFDRLGV
C	150 HIRSVWKDLLEDTET
C	151 IDTTIMGNEVFCVG
C	152 VMGSSYGFGVSPGQR
C	153 DCTMLVCGDDLVVIC

Peptide ID	
C	154 DCTMLVNGDDLVVIC
C	155 DPTMLVCGDDLVVIC
C	156 DPTMLVNGDDLVVIC
C1	157 LWARMMLMTHFFSIL
C	158 LVWRMVLMTHFFSIL
C	159 DLPQIHERLHGLSAF
C	160 DLPQIKRLHGLSAF
C	161 AVRTKLKLTPIPAAS
C	162 AVRTLKLKLTPLPAAS
C	163 SGGDIYHSVSRARPR
C	164 SGGDPYHSVSRARPR
C	165 WGENETDVLLLNNTR
C	166 GENETDVLLLNNTRP
C	167 WFGCTVWNNSTGFTKT
C	168 GCTWWNNSTGFTKTC
C	169 GCTWMNSTGFTKTCG
C	170 GLPVSARRGREILLG
C	171 LPVSARRGREILLGP
C	172 PVSARRGREILLGPA
C	173 VSARRGREILLGPAD
C	174 GLPVSALRGREILLG
C	175 LPVSALRGREILLGP
C	176 PVSALRGREILLGPA
C	177 VSALRGREILLGPAD
C	178 PDRGVLVREFDEMEEC
C	179 GNDEVLVREFDEMEEC
C	180 REVLYREFDEMEECA
C	181 EVLYREFDEMEECAS
C	182 VLYREFDEMEECASH
C	183 LYREFDEMEECASHL
C	184 YYLTRDPTTPLARAA
C	185 YLTRDPTTPLARAAW
C	186 LTRDPTTPLARAAWE
C	187 TRDPTTPLARAAWET
C	188 RDPTTPLARAAWETA
C	189 DPTTPLARAAWETAR
C	190 PTTPLARAAWETARH
C	191 YLTRDPTTPLARAA
C	192 YLTRDPTTPLARAAW
C	193 LTRDPTTPLARAAWE
C	194 TRDPTTPLARAAWET
C	195 RDPTTPLARAAWETV
C	196 DPTTPLARAAWETVR
C	197 PTTPLARAAWETVRH

Peptide ID [lpep]	
1506	MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVVLLPRRGPRLGVRATRKTSERSQPRGRRQPIPK
1526	VNLLPAILSPGALVVGVVCAAILRRHVGPGEGAVQWMNRLIAFASRGNHVSPTHYV
1545	IKGGRHLIFCHSKKKCDELA
1546	TVPQCAWSRSQRRGRTGRGR
1547	VLVAYQATVCARAQAPPPSWD
1551	HLHAPTGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAY
1552	YLHAPTGSGKSTKVPVAYAAQGYKVLVLNPSVAATLGFGAY
1553	GAAVGSIGLGKVLVDILAGYGAGVAGALVAFKIMSGE
1554	GAAVGSIGLGKVLVDILAGYGAGVAGALVAFKVMSGE
1555	GAAVGSIGLGKVLVDILAGYGAGISGALVAFKIMSGE
1556	FTEAMTRYSAPPGDPP
1557	SSMPPLEGSPGDFDL
1558	CGYRRCRASSGVLTTS
1559	PVNSWLGNIIMYAPT
1560	PVNSWLGNIIQYAPT
1561	SGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY
1562	SGMFDSSVLCECYDAGCAWYELTPAETSVRLRAY
1563	SGMFDSVVLCECYDAGAAWYELTPAETTVRLRAY
1564	SGMFDSVVLCECYDAGAAWYELTPAETSVRLRAY
1565	PWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF
1577	QEVQVVSTATGSFLAT
1578	QEVQVLSTVTQSFLGT
1579	FTDNSSPPAVPQTFQV
1580	FSDNSTPPAVPQTYQV
1581	NAVAYYRGLDVSVIPT
1587	VNLLPGILSPGALVVGVICAAILRRHVGPGEGAVQWMNRLIAFASRGNHVAPTHYV
1588	TTILGIGTVLDQAETAGARLVVLATATPPGSVT
1589	TSILGIGTVLDQAETAGARLVVLATATPPGSVT
1590	TSILGIGTVLDQAETAGVRLTVLATATPPGSVT
1591	TTILGIGTVLDQAETAGVRLTVLATATPPGSVT
1592	PWAKHMWNFISGIQYLAGLSTLPGNPAVASMAAF
1603	VFTGLTHIDAHFLSQTKQ
1604	VVCCSMSYTWTGALITPC
1605	VVCCSMSYSWTGALITPC
1606	VLTSMLTDPSHITAETA
1607	VLTSMLTDPSHITAEAA
1613	ASSSASQLSAPSLRATCTT
1614	LTPPHSARSKFGYGAKDVR
1615	LTPPHSAKSKFGYGAKDVR
1616	LTPPHSAKSKYGYGAKEVR
1617	LTPPHSARSKYGYGAKEVR
1618	PMGFSYDTRCFDSTVTE
1619	PMGFAYDTRCFDSTVTE
1620	TGDFDSVIDCNTCVTQ
1621	TGDFDSVIDCNVAVTQ
1622	NTPGLPVCQDHLEPWE
1623	YLVAYQATVCARAKAPPPSWD
1624	LECRDRSELSPLLLSTTEW
1625	LEDRDRSQLSPLLHSTTEW
1626	ASSSASQLSAPSLKATCTT
1627	PEYDLELITSCSSNVSVA
1628	VCGPVYCFTPSPVVVGTTDR
1629	GVAGWLSPRGSRPSWGP
1630	LLFLLLADARVCACLWM
1631	SGHRMAWDMMMNWSPT
1632	TGHRMAWDMMMNWSPT
1641	ITYSTYGKFLADGGCSGGAYDIIICDECHS
1647	ARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSC
1648	DPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGG
1649	DPRHRSRNVGKVIDTLTCGFADLMGYPVVGAPLGG
1650	VDYPYRLWHYPCTVNFTIFKVRMYVGGVEHRL
1651	VDYPYRLWHYPCTVNYTIFKIRMYVGGVEHRL
1652	KGGRKPARLIVFPDLGVRVCEKMALYDV
1653	KGGRKKAARLIVYPDLGVRVCEKMALYDV
1654	IQLINTNGSWHINRTALNCNDSL
1655	IQLVNTNGSWHINRTALNCNDSL
1656	LPALSTGLIHLHQNIVDVQYLYG

For epitope capture, each peptide pool was incubated with soluble recombinant HLA-class II molecules and specific binding was assessed by an SDS-stability assay. The results using the HLA molecules DRB1*0401, DRB1*0404 and DRB1*0101 are shown in Fig. 2 and 3 respectively: 28 peptide pools were found which bind to DRB1*0401 molecules: no. 1, 2, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20 from "row" pools and no. 23, 25, 26, 27, 29,30, 31, 34, 36, 38, 39 and 40 from "column" pools (Fig. 2). 35 peptide pools out of 40 tested were positive in binding to DRB1*0404 molecules (Fig. 3), while all peptide pools showed binding activity to DRB1*0101 molecules. By finding the intersections of reactive pools in the array, potential individual binders were determined and re-checked for binding affinity individually.

All individually confirmed peptides are summarized in Table 2. Binding to DRB1*0401 is shown in Fig. 4: 54 individual peptides were identified as ligands of this HLA-type. Often several overlapping 15mers in a row bound to HLA allowing identification of their core binding regions. Peptide differing only by one or two amino acids representing variants (see Table 1) usually bound both to soluble HLA class II molecules. Such "duplicates" were considered to represent the same epitope. Thus, 31 ligands capable to bind to DRB1*0401 were identified, including 11 previously known class II epitopes. From the latter, however, only two (A202-A206 and B60-B68) had been known to be restricted to DR4 (see Table 2). 20 ligands are candidates for novel epitopes. For DRB1*0404, 64 binders designated as 28 potential epitopes were determined, 4 of them belong to already known epitopes (Fig. 5, Table 2). For DRB1*0101, 83 peptides representing 44 potential epitopes were identified (Fig. 6, Table 2). Of those, 7 had been described previously but with different HLA restriction.

All individually confirmed peptides binding to at least one of the 3 above mentioned HLA types were also tested for affinity to DRB1*0701 molecules in a peptide-competition assay (Fig. 7, Table 2). Here, 50 ligands were identified. Of those, 7 correspond to already known class II epitopes, but only one was described as DRB1*0701epitope (A202-A206).

Table 2. HCV derived peptides binding to soluble HLA class II molecules. About 400 15- to 23-mer pepides derived from conserved regions of HCV were analyzed by the Epitope Capture Method using pools of up to 20 peptides arrayed in matrix format (see Fig. 1) and four different HLA class II molecules. Specific binding was confirmed for individual peptides.

ID	Peptide sequence	Binding to DRB1				Known / new potential epitope, HLA coverage	
		*0101	*0401	*0404	*0701		
A120	NTNGSWHINRTALNC	*		*	nb		
A122	NGSWHINRTALNCND	*		*	*	new DRB1*0101, *0401, *0404, *0701:	45-55%
A124	SWHINRTALNCNDSL	*		*	*		
B25	DAGCAWYELTPAETS	***	*	***			
B26	AGCAWYELTPAETSV	***	***	***	nb		
B28	CAWYELTPAETSVRL	***	**	***	*	new DRB1*0101, *0401, *0404, *0701:	45-55%
B30	WYELTPAETSVRLRA	**	*	**	nb		
B46	AGAAWYELTPAETTV	***		***	nb		
B48	AAWYELTPAETTVRL	***		***	**	new DRB1*0101, *0401, *0404, *0701:	45-55%
B94	SSIGLGKVLVDILAG	*	*	*			
B86	IGLGKVLVDILAGYG	*	**	*	**	new DRB1*0101, *0401, *0404, *0701:	45-55%
B88	LGKVLVDILAGYGAG	*	**	*			
B92	LVDILAGYGAGVAGA	*	nb				
C106	TRVPYFVRAQGLIRA	*	*	*	*	new DRB1*0101, *0401, *0404, *0701:	45-55%
C113	TAYSQQTRGLLGCII	***	*				
C114	TAYSQQTRGLLGCIV	***	*	*	*	new DRB1*0101, *0401, *0404, *0701:	45-55%
1627	PEYDLELITCSSSNVSVA	***	***	***	**	new DRB1*0101, *0401, *0404, *0701:	45-55%
1628	VCGPVYCFTPSPVVVGTTDR	***	**	*	*	new DRB1*0101, *0401, *0404, *0701:	45-55%
1629	GWAGWLLSPRGSRPSWGP	*	*	**	*	new DRB1*0101, *0401, *0404, *0701:	45-55%
1604	VVCCSMSYTWTGALITPC	*		**	***	new DRB1*0101, *0401, *0404, *0701:	45-55%
1630	LLFLLLADARVCACLWM	*		nb	***	new DRB1*0101, *0401, *0701:	40-50%
C97	GVLFGLAYFSMVGNW	**	**	nb	**	new DRB1*0101, *0401, *0701:	40-50%
1547	YLVAYQATVCARAQAPPPSWD	***		nb	**	new DRB1*0101, *0401, *0701:	40-50%
B94	DILAGYGAGVAGALV	*	nb	nb	nb		
B95	ILAGYGAGVAGALVA	*	nb	nb			
B96	LAGYGAGVAGALVAF	**	**	nb	*	new DRB1*0101, *0401, *0701:	40-50%
B97	AGYGAGVAGALVAFK	*	nb	nb			
B98	GYGAGVAGALVAFKI	*	nb	nb	nb		
A272	ETAGVRLTVLATATP	*	*	nb			
A274	AGVRLTVLATATPPG	*	nb		nb	new DRB1*0101, *0401, *0701:	40-50%
A276	VRLTVLATATPPGSV		nb		*		
B120	AGISGALVAFKIMSG	*	nb	*	***	new DRB1*0101, *0404, *0701:	~45%
B122	VNLLPAILSPGALVV	*	nb	*	*	new DRB1*0101, *0404, *0701:	~45%
C108	HAGLRDLAVAVEPVV	*	nb	*	*	new DRB1*0101, *0404, *0701:	~45%
C134	TTLLFNILGGWVAAQ	**	nb	*	**	new DRB1*0101, *0404, *0701:	~45%
C152	VMGSSYGFQYSPGQR	*	nb	*	*	new DRB1*0101, *0404, *0701:	~45%
1606	VLTSMLTDPSHITAETA	nb	***	**	**	new DRB1*0401, *0404, *0701:	~45%
1607	VLTSMLTDPSHITAEAA	nb	***	**	*	new DRB1*0401, *0404, *0701:	~45%
1577	GEVQVVSTATQSFLAT	nb	*	***	***	new DRB1*0401, *0404, *0701:	~45%
1578	GEVQVLSTVTQSFLGT	nb	*	***	***	new DRB1*0401, *0404, *0701:	~45%
B50	AGAAWYELTPAETSV	***	***	***		new DRB1*0101, *0401, *0404:	~40%
B52	AAWYELTPAETSVRL	***	***	***	nb		
1623	YLVAYQATVCARAKAPPPSWD	*		**		new DRB1*0101, *0401, *0404:	~40%
C130	QTVDFSLDPTFTIET	**	***	**	nb	new DRB1*0101, *0401, *0404:	~40%
1603	VFTGLTHIDAHFLSQTKQ	***	nb	nb	*	new DRB1*0101, *0701:	~40%
C96	GVLAGLAYYSMVGNW	**	nb	nb	*	new DRB1*0101, *0701:	~40%

C191	YYLTRDPTTPLARAA	nb	***	nb	*	new DRB1*0401, *0701:	~40%
A216	SGKSTKVPVAYAAQG	nb	*	nb	nb		
A218	KSTKVPVAYAAQGYK	nb	*	nb			
A220	TKVPVAYAAQGYKVL	*	**	nb		new DRB1*0101, *0401:	~35%
A222	VPVAYAAQGYKVLVL	*	nb	nb	nb		
A224	VAYAAQGYKVLVLNP	*	nb	nb			
A242	TILGIGTVLDQAETA	nb	nb				
A244	LGIGTVLDQAETAGA	*	*	nb	nb	new DRB1*0101, *0401:	~35%
C92	AFCSAMYVGDLCGSV	*	**	nb	nb	new DRB1*0101, *0401:	~35%
C93	AFCSALYVGDLCGSV	*	*	nb			
A174	PALSTGLLHLHQNIV		nb	*	*	new DRB1*0404, *0701:	25-30%
B32	SGMFDSVVLCEGYDA	*	nb	***			
B34	MFDSVVLCEGYDAGA	*	nb	***	nb	new DRB1*0101, *0404:	20-25%
B36	DSVVLCEGYDAGAAW	*	nb	***			
B38	VVLCEGYDAGAAVYE	nb	nb	*	nb		
B100	GAGVAGALVAFKIMS	**	nb	**		new DRB1*0101, *0404:	20-25%
B102	GVAGALVAFKIMSGE	***	nb	***			
C135	TTLLLNILGGWLAAQ	**	nb	*		new DRB1*0101, *0404:	20-25%
C162	AVRTKLKLTPLPAAS	nb	*	*	nb	new DRB1*0401, *0404:	20-25%
1618	PMGFSYDTRCFDSTVTE	nb	nb		**	new DRB1*0701:	~25%
1622	NTPGLPVCQDHLEFWE	nb	nb		***	new DRB1*0701:	~25%
1624	LEDRDRSELSPLLLSTTFW	nb	nb		*	new DRB1*0701:	~25%
1546	TVPQDAVSRSQRRGRTGRGR	nb	nb	nb	*	new DRB1*0701:	~25%
1556	FTEAMTRYSAPPGDPP	nb	nb	nb	*	new DRB1*0701:	~25%
A114	LPGCSFSIFLLALLS	**	nb	nb	nb	new DRB1*0101:	~20%
B58	MWNFISGIQYLAGLS	*	nb	nb		new DRB1*0101:	~20%
B112	VDILAGYGAGISGAL	*	[redacted]				
B114	LAGYGAGISGALVA	***	[redacted]			new DRB1*0101:	~20%
B116	AGYGAGISGALVAFK	***	[redacted]	nb	nb		
B118	YGAGISGALVAFKIM	***	[redacted]	nb			
B18	DAGCAWYELTPAETT	***		nb	nb		
B20	GCAWYELTPAETTVR	***	nb			new DRB1*0101:	~20%
B22	AWYELTPAETTVRLR	**		nb	nb		
C112	GQGWRLLAPITAYSQ	**	nb			new DRB1*0101:	~20%
C116	GCIVVSMTGRDKTQV	*	nb	nb		new DRB1*0101:	~20%
C122	SYLKGSSGGPLLCPS	*	nb	nb		new DRB1*0101:	~20%
C127	TGEIPFYGKAIPIEV	*	nb			new DRB1*0101:	~20%
C144	FFTWLDGVDIHRYAP	**	nb	nb		new DRB1*0101:	~20%
C159	DLPQIIERLHGLSAF	*	nb	nb	nb	new DRB1*0101:	~20%
C160	DLPQIIQRLHGLSAF	*	nb				
C174	GLPVSALRGREILLG	*	nb	nb		new DRB1*0101:	~20%
1558	CGYRRCRASGVLTTS	***	[redacted]	nb	nb	new DRB1*0101:	~20%
1581	NAVAYYRGLDVSVIPT	**	nb	nb	nb	new DRB1*0101:	~20%
C95	EFVQDCNCSIYPGHV	nb	**	nb	nb	new DRB1*0401:	~20%
C129	PTSGDVVVVATDALM	nb	nb	**		new DRB1*0404:	~5%
C157	LWARMILMTHFFSIL	nb	nb	*	nb	new DRB1*0404:	~5%
C158	LWVRMVLMTHFFSIL		nb	*			
A254	ETAGARLVVLATATP	nb	nb	*			
A256	AGARLVVLATATPPG	nb	nb	*		new DRB1*0404:	~5%
A258	ARLVVLATATPPGSV	nb	nb	**			
1605	VVCCSMSYSWTGALITPC	nb	nb	*	nb	new DRB1*0404:	~5%
C109	AAGLRDLAVAVEPIV		nb	*		new DRB1*0404:	~5%
C161	AVRTKLKLTPIPAAS		nb	*		new DRB1*0404:	~5%
A60	LGKVIDTLTCGFA	**	nb	nb	**	known DR4, DR8, DR15	

A61	GKVIDTLTCGFAD	**				new DR*0101, 0701
A70	TCGFADLMGYIPLVG	*	nb	nb		
A72	GFADLMGYIPLVGAP	***	*	**		known class II
A74	ADLMGYIPLVGAPLG	***		***	**	DR*0101,0404, 0701
A88	CGFADLMGYIPVVGA	**		**	*	
A90	FADLMGYIPVVGAPL	***		***		known class II
A92	DLMGYIPVVGAPLGG	***	nb	***	***	DR*0101, 0404, 0701
A96	LAHGVRVLEDGVNYA	nb	***	nb		
A98	HGVRVLEDGVNYATG	nb	***	***	**	known DR11
A100	VRVLEDGVNYATGNL	nb	***	***	*	new DR*0401, 0404, 0701
A102	VLEDGVNYATGNLPG	nb		*		
A104	EDGVNYATGNLPGCS	nb	*	nb	nb	
A200	AAQGYKVLVLNPSVA		nb	***	**	
A202	QGYKVLVLNPSVAAT	***	***	***	***	known DRB1*0401, 0701, DR11, DR15
A204	YKVLVLNPSVAATLG	***	***	***	***	new DR*0101
A206	VLVLNPSVAATLGFG	***	***	***	***	
C30	AVQWMNRLIAFASRG	*	nb	nb		known DR11, DQ5, also DR*0101
B60	NFISGIQYLAGLSTL	**	*	nb	*	
B62	ISGIQYLAGLSTLPG	***	***	***	**	
B64	GIQYLAGLSTLPGNP	***	***	***	**	known DR*0401, 1101
B66	QYLAGLSTLPGNPAI	*	***	***	**	new 0101, 0404, 0701
B68	LAGLSTLPGNPAIAS	*	*	***	**	
C124	GHAVGIFRAAVCTRG	**	*	nb	**	known DR*0101,0401, 0701
1620	TGDFDSVIDCNTCVTQ	nb	nb	*		new DR*0404
1621	TGDFDSVIDCNVAVTQ	*	nb	nb	nb	known DR13, also DR*0101, 0401
1631	SGHRMAWDMMMNWSPT	nb			nb	known class II, also DR*0401
1632	TGHRMAWDMMMNWSPT	nb	*			known class II, also DR*0401

*** strong binding
** intermediate binding
* weak binding
nb no binding

Boldface peptide IDs indicate HLA-ligands with confirmed immunogenicity in HLA-transgenic mice

Boldface peptide sequences indicate putative core binding regions based on prediction algorithms as described in the text.

[1)] immunogenic in DRB1*0401 transgenic mice

Some of the highly promiscuous peptides and/or with computer algorithm (SYFPEITHI, TEPITOPE)-predicted affinities were checked for binding to soluble HLA-DRB1*1101 molecules in a peptide-competition assay as it is described for HLA-DRB1*0701. Several known DR11 epitopes were used as controls and were confirmed to bind HLA-DRB1*1101 molecules in vitro. Among newly identified HLA-DRB1*1101 binders, there are peptides with IDs A120, A122, A141, C114, C134, 1426, 1628, 1629 of high affinity, 5 peptides with IDs C106, C135, 1578, 1547, 1604 of moderate affinity and 4 peptides with IDs B46, B48, B86, B96 of weak affinity ligands.

In summary eight novel ligands binding at least to HLA-DRB1*0101, *0401, *0404, *0701 and *1101 (Tab. 2: peptide Ids A120, A122, A141, 1604, 1547, 1628, 1629,and Tab. 6: peptide ID 1426); novel 10 ligands binding at least to HLA-DRB1*0101, *0401, *0404 and *0701 (Tab. 2: peptide IDs A120-A124, B25-B30, B46-B48, B84-B92, C106, C113-C114, 1627, 1628, 1629, 1604); 5 novel ligands binding at least to HLA-DRB1*0101, *0401 and *0701, 5 novel ligands binding at least to HLA-DRB1*0101, *0404 and *0701, 4 novel ligands binding at least to HLA-DRB1*0401, *0404 and *0701, 3 novel ligands binding at least to HLA-DRB1*0101, *0401 and *0404, 2 novel ligands binding at least to HLA-DRB1*0101 and *0701, 1 novel ligand binding at least to HLA-DRB1*0401 and *0701, 3 novel ligands binding at least to HLA-DRB1*0101, *0401, 1 novel ligand binding at least to HLA-DRB1*0404 and *0701, 4 novel ligand binding at least to HLA-DRB1*0101 and *0404, 5 novel ligands binding at least to HLA-DRB1*0701, 13 novel ligands binding at least to HLA-DRB1*0101, 1 novel ligand binding at least to HLA-DRB1*0401, and 6 novel ligands binding at least to HLA-DRB1*0404.

Moreover, 12 known HLA class II epitopes were confirmed, in several cases binding to alleles not reported yet was demonstrated (Tab. 2, last group).

Having established physical binding too HLA class II it is straightforward to verify immunogenicity for a given ligand: for instance peptide IDs A120-A124, B46-B48, 1627, 1604, 1630, 1547, 1623, B112-118, 1558, all binding to one or more HLA class II alleles were also shown to be immunogenic in HLA-DRB1*0401

transgenic mice (see Example II).

To determine the optimal epitope within a longer polypeptide, mice can be vaccinated with a longer polypeptide incorporating the candidate epitope sequences. Generation of specific CD4+ T cell responses against naturally processed and presented epitopes can then be assayed by re-stimulation of murine splenocytes or lymph node cells with overlapping 15-mers and IFN-gamma ELIspot. Final confirmation/validation of the newly identified HLA-ligands can be achieved by testing these peptides with T-cells from humans. Ideally, these comprise therapy responders or subjects spontaneously recovered from infection.

Example II. Immunogenicity of HCV-derived peptides in HLA-transgenic mice

Synthetic HCV-derived peptides (from conserved regions) were investigated for immunogenicity in HLA-transgenic mice: 36 of 68 peptides tested were found to induce peptide-specific IFN-gamma-producing cells in vaccination experiments. As summarized in Table 3, some peptides were either immunogenic (+, less than 100 peptide-specific cells among a million splenocytes) or even strongly immunogenic (++, more than 100 peptide-specific cells among a million splenocytes) in DR4- and/or A*0201-transgenic mice.

Table 3:

Ipep	DR1*0401	A*0201	B*0702	Sequence
1506			+	MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQ-PRGRRQPIPK
1526	+	+	+	VNLLPAILSPGALVVGVVCAALLRRHVGPGEGAVQWMNRLIAFASRGNHVSPTHYV
1545		+		IKGGRHLIFCHSKKKCDELA
1547	++		+++	YLVAYQATVCARAQAPPPSWD
1552		+	+	YLHAPTGSGKSTKVPVAYAAQGYKVLVLNPSVAATLGFGAY
1553		+	+	GAAVGSIGLGKVLVDILAGYGAGVAGALVAFKIMSGE
1555	+	+	+	GAAVGSIGLGKVLVDILAGYGAGISGALVAFKIMSGE

1558	++	+	++	CGYRRCRASGVLFTS
1559	+	++		PVNSWLGNIIMYAPT
1560	+	++		PVNSWLGNIIQYAPT
1562			+	SGMFDSSVLCECYDAGCAWYELTPAETSVRLRAY
1563	+		+	SGMFDSVVLCECYDAGAAWYELTPAETTVRLRAY
1565	++	++	+	FWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF
1577		+	+	GEVQVVSTATQSFLAT
1578			+	GEVQVLSTVTQSFLGT
1580			+	FSDNSTPPAVPQYTQV
1587		+	+	VNLLPGILSPGALVVGVICAAILRRHVGPGEGAVQWMNRLIAFASRGNHVAPTSYV
1592	++	++	+	FWAKHMWNFISGIQYLAGLSTLPGNPAVASMHAF
1604	++	++	++	VVCCSMSYTWTGALITPC
1605	+	+	+	VVCCSMSYSWTGALITPC
1615		+		LTPPHSAKSKPGTGAKDVR
1616	+			LTPPHSAKSKYGYGAKEVR
1617		+		LTPPHSARSKYGYGAKEVR
1621	+	+	+	TGDFDSVIDCNVAVTQ
1623	+	+	+	YLVAYQATVCARAKAPPPSWD
1624			+	LEDRDRSELSPLLLSTTEW
1625	+			LEDRDRSQLSPLLLSTTEW
1627	+	+	++	PEYDLELITSCSSNVSVA
1628			++	VCGPVYCFTPSPVVVGTTDR
1630	++	++		LLPLLLADARVCACLWM
1631	+	+		SGHRMAWDMMMNWSPT
1632		+		TGHRMAWDMMMNWSPT
1641		+		ITTSTYGKPLADGGCSGGAYDIIICDECHS
1647		+	+	ARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSC
1649	+			DPRHRSRSVGKVIDTLTCGFADLMGYIPVVGAPLGG
1650	++	++	+	VDYFYRLWHYPCTVNFTIFKVRMYVGGVEHRL
1651	++	++	+	VDYFYRLWHYPCTVNYTIFKIRMYVGGVEHRL
1652	++	+		KGGRKPARLIVFPDLGVRVCEKMALYDV
1653		+		KGGKKAARLIVYPDLGVRVCEKMALYDV
1654	++	+		IQLINTNGSWHINRTALNCNDSL
1655	++	+		IQLVNTNGSWHINRTALNCNDSL
1656	+			LPALSTGLIHLHQNIVDVQYLYG

Peptide 1526, 1565, 1631, also shown to be immunogenic in HLA-DRB1*0401 transgenic mice contain known class II epitopes. Peptide IDs 1526, 1553, 1565, 1587, 1623, 1630 also shown to be

immunogenic in HLA-A*0201 transgenic mice contain known A2 epitopes.

For further characterizing the novel epitopes provided herewith, one may define the exact HLA restriction of these epitopes and the minimal epitopes within the sequences recognized by T cells. Both can be done by a variety of well-established approaches known to the one skilled in the art (Current Protocols in Immunology, John Wiley& Sons, Inc.).

First, publicly available programs can be used to predict T cell epitopes on the basis of binding motifs. These include for instance: http://bimas.dcrt.nih.gov/molbio/hla_bind/ (Parker et al. 1994), http://134.2.96.221/scripts/MHCServer.dll/home.htm (Rammensee at al. 1999), http://mypage.ihost.com/usinet.hamme76/ (Sturniolo et al. 1999). The latter prediction algorithm offers the possibility to identify promiscuous T helper-epitopes, i.e. peptides that bind to several HLA class II molecules. These predictions can be verified by testing of binding of the peptide to the respective HLA.

A way of quickly discerning whether the response towards a peptide is class I or class II restricted is to repeat the ELIspot assay with pure CD4+ or CD8+ T cell effector populations. This can for instance be achieved by isolation of the respective subset by means of magnetic cell sorting. Pure CD8+ T cells can also be tested in ELIspot assays together with artificial antigen-presenting-cells, expressing only one HLA molecule of interest. One example are HLA-A*0201 positive T2 cells (174CEM.T2, Nijman et al., 1993). Alternatively, one can use ELIspot assays with whole PBMCs in the presence of monoclonal antibodies specifically blocking either the CD4+ or CD8+ T cell sub-population. Exact HLA restriction can be determined in a similar way, using blocking monoclonal antibodies specific for a certain allele. For example the response against an HLA-A24 restricted epitope can be specifically blocked by addition of an HLA-A24 specific monoclonal antibody.

For definition of the minimal epitopes within the peptide sequences recognized by T cells, one can test overlapping and

truncated peptides (e.g. 8-, 9-, 10-mers) with splenocytes from immunized transgenic mice or T-cells from humans recognizing the respective epitope.

Example III. HLA restriction of immunogenic HCV-derived peptides investigated in transgenic mice.

Groups of 5 mice (HLA-A*0201-, HLA-DRB1*0401- and HLA-B*0702 transgenic mice, male, 8-14 weeks of age) were injected subcutaneous into the hind footpads with 100µg of peptide + IC31 per mouse (50µg per footpad). (PCT/EP01/12041, WO 02/32451 A1 and PCT/EP01/06433, WO 01/93905 A1; IC31 is a combination of the immunizer disclosed in WO 01/93905 and WO 02/32451).

6 days after vaccination single cell suspension of pooled spleens were prepared and additionally pure fractions of CD8+ in the case of A2 and B7 tg mice (CD8+ fraction for B7 mice containing 97% of CD8 and 1.5% of CD4 cells and for A2 tg mice 83% of CD8 and 8% of CD4 cells) and CD4+ for DR4tg mice (CD4+ fraction for DR4tg mice containing 98% of CD4 cells and 0.2 % of CD8 cells) were separated from the spleen cell suspension using *MACS* separating kit (Miltenyi, Germany). All cells (not separated cells, positive and corresponding negative fractions) were restimulated *ex vivo* with relevant peptide (for instance Ipep1604) and irrelevant peptides as negative control (known HLA-DRB1*0401 CMV-derived epitope Ipep 1505, HLA-B*0702 HIV-derived epitope Ipep 1787, or HLA-A*0201 tyrosinase-derived epitope Ipep1124) to detect INF-γproducing cells in ELISpot assay.

As an example shown in Fig. 8-10 the Ipep1604 (VVCCSMSYTWTGALITPC, in combination with immunizer IC31) was able to induce high numbers of specific INF-γproducing T cells in all three transgenic class I and II mouse strains. This was shown not only with whole spleen derived cells but also with enriched fractions of CD8+ cells correspondingly for A2 and B7 and CD4+ cells for DR4tg mice. Similar, albeit weaker responses were seen with Ipep1605 (VVCCSMSYSWTGALITPC), a sequence variant with a serine instead of a threonine.

Thus, Ipep1604 contains class I epitopes for HLA-A*0201 and HLA-B*0702 and a class II epitope for HLA-DRB1*0401 molecules.

As shown in Tables 2 and 6, Ipep 1604 binds to class II molecules in a promiscuous manner. Thus, it contains further epitopes, at least for HLA-DRB1*0101, DRB1*0404, DRB1*0701 and DRB1*1101.

Other peptides were analysed in a similar way:
Ipeps 1605, 1623, 1547, 1558, 1559, 1560, 1565, 1592, 1650, 1654 and 1655 were confirmed to contain human HLA-DRB1*0401 epitopes. Again, for most of these epitopes binding is not limited to HLA-DRB1*0401 as shown in Tables 2 and 6.

Ipeps 1565, 1605 and 1650 were confirmed to contain human HLA-A*0201 epitopes.

Ipeps 1506, 1587 were confirmed to contain human HLA-B*0702 epitopes.
Ipep 1843 with sequence LPRRGPRL was shown to be the HLA-B*0702 minimal epitope contained in 1506:
Fig. 10 shows mouse IFN-gamma ELIspot with splenocytes or separated CD8+ or CD4+ cells from HLA-A*0702 transgenic mice vaccinated with Ipep1506+IC31 or Ipep1835+IC31.

Fig. 10 A) and B) shows that after a single vaccination with either Ipep 1506+IC31 or Ipep1835+IC31, upon restimulation with overlapping 15mers, the 15mers A30 to A37 (see Tab.1) react. The common sequence of these 15mers is LPRRGPRL (Ipep 1843, see Tab.4).

Fig. 10 C) confirms these findings: after a single vaccination with either Ipep1506+IC31 or Ipep1835+IC31, significant interferon-gamma induction against Ipep1843 can be detected. In both cases Ipep 1790 an HIV NEF-derived HLA-B*0702 epitope (sequence RPMTYKAAL was used as negative control for restimulation.

Ipep 1838 with sequence SPGALVVGVI (see Tab.4) was shown to be an HLA-B*0702 minimal epitope contained in 1587:
In the case of Ipep1587 a different approach was taken: the sequence of Ipep1587 was inspected for HLA-B*0702 binding motifs and a couple of short peptides were synthesized accordingly.

These were tested in a competition-type peptide binding assay using soluble HLA-B*0702 and the FITC-labelled reference peptide LPCVLWPVL, which is a known HLA-B*0702 epitope derived from EBV (Stuber et al., 1995). Peptide Ipep1838 showed ~30% competition when used in 80-fold molar excess for 48h at 37°C. Thus it is likely to present the minimal HLA-B*0702 epitope contained in Ipep 1587.

Example IV: Identification and confirmation of novel HCV peptides reactive in IFN-gamma ELIspot with human PBMC from HCV therapy responders or patients with spontaneous recovery

40 peptide mixtures in matrix format (Fig. 1) containing synthetic peptides derived from conserved regions of HCV (Table 1) were screened in IFN-gamma ELIspot using PBMC from more than 50 individuals who were either responders to interferon/ribavirin standard therapy, or, who had spontaneously cleared HCV (i.e. all subjects were HCV antibody positive, but HCV-RNA negative). PBMC from such individuals are supposed to contain the relevant T-cell populations responsible for clearing HCV. Thus, peptides discovered or confirmed by using these PBMC are likely to represent the structural determinants of immune protection against/clearance of HCV.Based on the results from this primary matrix-screen, a number of peptides were chosen for individual re-testing in IFN-gamma ELIspot using PBMC from selected donors. In addition, several new peptides incorporating sequences from overlapping reactive peptides or avoiding critical residues like cystein were synthesized. These are summarized in **Table 4.**

Table 4: additional peptides derived from conserved regions of HCV.

Peptide ID	**Peptide sequence (1 amino acid code)**
1006	MWNFISGIQYLAGLSTLPGN
1334	HMWNFISGI
1425	NFISGIQYLAGLSTLPGNPA
1426	HMWNFISGIQYLAGLSTLPGNPA
1798	IGLGKVLVDILAGYGAGVAGALVAFK
1799	AAWYELTPAETTVRLR
1800	DYPYRLWHYPCTVNYTIFKI
1836	DYPYRLWHYPCTVNFTIFKI

1801	AYSQQTRGLL
1827	TAYSQQTRGLLG
1829	SMSYTWTGALITP
1838	SPGALVVGVI
1843	LPRRGPRL

Results of the secondary screening with individual peptides are summarized in **Table 5.** Altogether ~20% of subjects (G05, G18, H02, H03, H04, H10, H12, H19, H32, H38) showed a significant IFN-gamma T-cell response against one ore more of the peptides. In some cases the observed number of ELIspots was clearly elevated, but not statistically significant above background. In these cases, PBMC (donors H03, H10, H33, H38) were stimulated with the respective peptides in vitro (2 rounds of in vitro priming, see Material & Methods) in order to increase the peptide specific response. Several peptides were confirmed in this way, results are again summarized in Table **5.**

Peptides A3-A7 represent overlapping 15mers spanning the sequence TNPKPQRKTKRNTNRRPQD. Since they all react with PBMC from donor H03, the minimal sequence of the epitope is located within the sequence PQRKTKRNTNR. Prediction algorithms indicate that QRKTKRNTN and QRKTKRNT represent ligands of HLA-B*08, whereas RKTKRNTNR most probably binds to HLA-B*2705.
Peptides C64-C70 represent overlapping 15mers spanning the sequence KGGRKPARLIVFPDLGVRVCE. C64 and C70 react with PBMC from donor H32 and H38, respectively. The minimal sequence of the epitope is therefore located within the sequence ARLIVFPDL. Prediction algorithms indicate that ARLIVFPDL represents a ligand of HLA- HLA-B*2705 and HLA-B*2709.

Table 5. Summary of HCV peptides reactive with PBMC.
Numbers represent peptide-specific IFN-gamma secreting T-cells/10^6 PBMC calculated from ELIspot results (duplicate determinations); values > 8 (>3x over background) were regarded statistically significant. Donors H32 and H33 are spontaneously recovered patients.

	Donors reactive directly ex vivo in IFN-gamma ELIspot with HCV-derived peptides										reactive after 2 rounds of in vitro stimulation			
Peptide ID	G05	G18	H02	H03	H04	H10	H12	H19	H32 SPR	H38	H03	H10	H33 SPR	H38
1557				20							75			
1577			15		30								165	
1579			45		35						75			
1605					25									
1615				30							325			
1624	30		55		30			420						
1628			40		45		25			20				100
1629			30		70		15							
1798					25							115		
1799							20					90		
1800										35		95		
1801						20				20				
A3											80			
A4				15										
A5											110			
A7											70			
A78					25									
A170					35									
A212					60									
A241					35									
B08					55									
B38									30					
B76					35									
C64									30					
C70										20				
C92					25									
C94					25									
C97					35									
C98					70									
C100		60			70									
C101					50									
C102				20										
C106					45									
C112					20									

C118				35										
C120				25	45						105			
C134					20									
C138													30	

	Donors reactive directly ex vivo in IFN-gamma ELIspot with HCV-derived peptides										reactive after 2 rounds of in vitro stimulation		
Peptide ID	G05	G18	H02	H03	H04	H10	H12	H19	H32 SPR	H38	H03	H10	H33 SPR
1557				20							75		
1577			15		30								165
1579			45		35						75		
1605					25								
1615				30							325		
1624	30		55		30			420					
1628			40		45		25			20			
1629			30		70		15						
1798					25							115	
1799							20					90	
1800										35		95	
1801						20				20			
A3											80		
A4				15									
A5											110		
A7											70		
A78					25								
A170					35								
A212					60								
A241					35								
B08					55								
B38									30				
B76					35								
C64									30				
C70										20			
C92					25								
C94					25								
C97					35								
C98					70								
C100		60			70								

C101					50							
C102				20								
C106					45							
C112					20							
C118				35								
C120				25	45						105	

Example V. Binding of HCV derived peptides to HLA class II molecules

In addition to the peptides listed in Table 1, several new peptides incorporating sequences from overlapping reactive peptides or avoiding critical residues like cystein were synthesized **(Table 4)**. These were retested for their affinities to class II soluble HLA molecules, and results were compared to those obtained with the original (Table 6).

Table 6. Binding of selected HCV-derived peptides and their 15-mer counterparts to soluble HLA class II molecules ("+++" strong affinity, "++" intermediate affinity, "+" weak affinity, "-" no affinity, "nd" not done; core binding motifs are underlined).

Peptide ID	Peptide sequences	Binding to soluble HLA-DRB1*				
		0101	**0401**	**0404**	**0701**	**1101**
1798	IGLGKVLVDILAGYGAGVAGALVAFK	-	-	+	++	+/-
B84	GSIGLGKVLVDILAG	+	+	+		-
B86	IGLGKVLVDILAGYG	+	++	+	+	+/-
B88	LGKVLVDILAGYGAG	+	++	+		
B92	LVDILAGYGAGVAGA	+	-			
B94	DILAGYGAGVAGALV	+	-	-	-	
B96	LAGYGAGVAGALVAF	++	++	-	+/-	+/-
1799	AAWYELTPAETTVRLR	+++	+	+	-	+/-
B46	AGAAWYELTPAETTV	+++	+++	+++	-	+/-
B48	AAWYELTPAETTVRL	+++	+++	+++	-	+/-
1827	TAYSQQTRGLLG	++	-	+/-	+	+
C114	TAYSQQTRGLLGCIV	+++	+/-	+/-	+	++
1829	SMSYTWTGALITP	+	-	-	+	+/-
1604	VVCCSMSYTWTGALITPC	+	+	++	++	+
1650	VDYPYRLWHYPCTVNFTIFKVRMYVGGVEHRL					
A130	DYPYRLWHYPCTVNF	+	++	+/-		
A131	YPYRLWHYPCTVNFT		-			
A135	**LWHYPCTVNFTIFKV**	-	-		++	

A141	TVNFTIFKVRMYVGG	-	-	+/-		++
A145	TIFKVRMYVGGVEHR	+/-	-			
1651	VDYPYRLWHYPCTVNYTIFKIRMYVGGVEHRL					
1800	DYPYRLWHYPCTVNYTIFKI	-	-	+/-	++	-
A147	DYPYRLWHYPCTVNY	-	-			
A152	LWHYPCTVNYTIFKI	-	-			
A158	TVNYTIFKIRMYVGG	-	-	+/-		
A162	TIFKIRMYVGGVEHR	+/-	-			
1817	RMYVGGVEHRL	-	-	+/-		
1426	HMWNFISGIQYLAGLSTLPGNPA	+	+	++	++	+
1425	NFISGIQYLAGLSTLPGNPA	++	++	++	nd	nd
1006	MWNFISGIQYLAGLSTLPGN	++	+	++	nd	nd

Abolished affinities to DRB1*0101 and DRB1*0401 molecules in the case of peptide 1798 in comparison with its shorter counterparts (B84 - B96) is probably due to the long sequence (26 amino acids) which can have a secondary structure that prevents binding. It is to be expected that in vivo, upon proteolytic cleavage, peptide 1798 will give rise to two shorter class II epitopes. Removed cystein (C) residues in peptides 1827 and 1829 (derivatives of peptides C114 and 1604, respectively) seem to be crucial for binding to DRB1*0401 molecules but do not essentially change affinities to other tested DR subtypes.

Example VI. Identification and Characterization of HCV-epitope hotspots

Here, a T-cell epitope hotspot (thereafter referred to as "hotspot") is defined as a short peptide sequence at least comprising more than one T-cell epitope. For example, two or more epitopes may be located shortly after each other (shortly being defined as less than 5-10 amino acids), or directly after each other, or partially or even fully over-lapping. Hotspots may contain only class I or class II epitopes, or a combination of both. Epitopes in hotspots may have different HLA restrictions.

Due to the highly complex and selective pathways of class I and class II antigen processing, referred to in the introduction, T-cell epitopes cannot be easily predicted within the sequence of a polypeptide. Though widely used, computer algorithms for T-cell epitope prediction have a high rate of both false-negatives and false-positives.

Thus, as even individual T-cell epitopes are not obvious within the sequence of a polypeptide, the same is even more the case for hotspots. Several radically different experimental approaches are combined according to the present invention for T-cell epitope identification, including epitope capture, HLA-transgenic animals and *in vitro* stimulation of human mononuclear cells. All three approaches are systematically applied on overlapping peptides spanning the antigen of interest, enabling comprehensive identification of epitopes (refer to CMV Epitope Capture patent). Upon such a comprehensive analysis, not limited to a particular HLA allele, but rather unravelling all possibly targeted epitopes within a population, epitope hotspots may become apparent. Within an antigen, only few if any sequences show characteristics of hotspots. Thus the identification of a hotspot is always a surprising event.

T-cell epitope hotspots offer important advantages: Hotspots can activate and can be recognized by different T-cell clones of a subject. Hotspots (when comprising epitopes with different HLA restriction) can interact with T-cells from different non HLA-matched individuals.

Epitope-based vaccines, so far have aimed at selected prevalent HLA-alleles, for instance HLA-A2, which is expressed in about half of Caucasians. Since other alleles are less frequent, epitope-based vaccines with broad worldwide population coverage will have to comprise many different epitopes. The number of chemical entities (for instance peptides) of a vaccine is limited by constraints originating from manufacturing, formulation and product stability.

Hotspots enable such epitope-based vaccines with broad worldwide population coverage, as they provide a potentially high number

of epitopes by a limited number of peptides.

Table 7: T-cell epitope hotspots in conserved regions of HCV. Hotspots (incl. some variations) are shown in bold, epitopes contained within the hotspots in normal font. Peptide number and sequence, as well as HLA-class I and class II coverage are given. Source data refers to Examples and Tables within this specification, or literature references.

peptide ID	peptide sequence	class I	class II	source data
1835	**KFPGGGQIVGGVYLLPRRGPRLGVRATRK**	**A2, A3, B7**	**DR11**	**Example III, VI**
83	**KFPGGGQIVGGVYLLPRRGPRL**	**A2 B7**	**DR11**	**Example VI**
1051	YLLPRRGPRL	A2		Bategav 1995
1843	LPRRGPRL	B7		Example III
	GPRLGVRAT	B7		Koziel 1993
	RLGVRATRK	A3		Chang 1999
84	GYKVLVLNPSVAAT		DR1,4,7,11	Tab.2:A200-A206
	AYAAQGYKVL	A24		prediction
84EX	**AYAAQGYKVLVLNPSVAAT**	**A24**	**DR1,4,7,11**	**Example VI**
87	DLMGYIPAV	A2		Sarobe 1998
	GYIPLVGAPL	A24		prediction
87EX	**DLMGYIPLVGAPL**	**A2,A24**		**Example VI**
89	CINGVCWTV	A2		Koziel 1995
1577	GEVQVVSTATQSFLAT		DR 4, 7	Tab.2
89EX	**GEVQVVSTATQSFLATCINGVCWTV**	**A2**	**DR 4, 7**	**Example VI**
1426	**HMWNFISGIQYLAGLSTLPGNPA**	**A2**	**DR1,4,7,11**	Example VII
1006	MWNFISGIQYLAGLSTLPGN			Example VII
1425	NFISGIQYLAGLSTLPGNPA			Example VII
	QYLAGLSTL	A24		prediction
1334	HMWNFISGI	A2		Wentworth 1996
1650	**VDYPYRLWHYPCTVNFTIFKVRMYVGGVEHRL**	**Cw7,A2,A24, A11,A3**	**DR1,4,7,11**	**Tab. 2,3,6 Example III**
1836	**DYPYRLWHYPCTVNFTIFKI**	**Cw7,A2;A24, A11**	**DR1,4,7,11**	**Tab. 2,3,6**
1846	**DYPYRLWHYPCTVNFTIFKV**	**Cw7,A2;A24, A11**	**DR1,4,7,11**	**Tab. 2,3,6 Example III**
1651	**VDYPYRLWHYPCTVNYTIFKIRMYVGGVEHRL**			**Tab. 2,3,6**
1800	**DYPYRLWHYPCTVNYTIFKI**	**Cw7,A24,A11**	**DR7**	**Tab. 2,5,6**
1754	DYPYRLWHY	Cw7		Lauer 2002
1815	TVNYTIFKI	A11		prediction

1816	TINYTIFK	A11		Koziel 1995
	TVNFTIFKV	A11		prediction
	HYPCTVNYTI	A24		prediction
	HYPCTVNFTI	A24		prediction
	RMYVGGVEHR	A3		Chang 1999
1799	**AAWYELTPAETTVRLR**	**B7? B35**	**DR1, 4**	**Tab. 2,5,6**
1818	TPAETTVRL	B7? B35		Ibe 1998
1827EX	**GWRLLAPITAYSQQTRGLLGCIV**	**A2,A3,A24, B8**	**DR1,4,7,11**	**Example VI**
C114	**TAYSQQTRGLLGCIV**	**A24, B8?**	**DR1,4,7,11**	Tab.2, 6
1827	**TAYSQQTRGLLG**	**A24, B8**	**DR1, 7,11**	Tab.6
C112	GQGWRLLAPITAYSQ	A3?,A2?,	DR1	Tab.2, 5
	RLLAPITAY	A3		prediction
C114EX	**GQGWRLLAPITAYSQQTRGLLGCIV**	**A24,A3?,A2?, B8?**	**DR1,4,7,11**	**Tab. 2, 5, 6**
		A24,A3?,A2?,	**DR1, 7,11**	**Tab. 2, 5, 6**
1827EX	**GQGWRLLAPITAYSQQTRGLLG**	**B8?**		
1801	AYSQQTRGLL	A24		Tab. 5
1819	AYSQQTRGL	A24		Kurokohchi 2001
1798	**IGLGKVLVDILAGYGAGVAGALVAFK**	**A2,24,3,11**	**DR1,4,7**	**Tab.2,3,5,6**
1820	ILAGYGAGV	A2		Bategay 1995
1821	VAGALVAFK	A3,11		Chang 1999
	GYGAGVAGAL	A24		prediction
1604	**VVCCSMSYTWTGALITPC**	**A2,A24,B7**	**DR1,4,7,11**	**Tab.2,3,6**
1829	**SMSYTWTGALITP**	**A2,A24,B7,**	**DR1, 7,11**	Tab.6
	SMSYTWTGAL	A2,B7		prediction
	SYTWTGALI	A24		prediction
1579	**FTDNSSPPAVPQTFQV**	**A1,2;B7,51**	**DR53=B4*01**	**Tab.5**
1624	**LEDRDRSELSPLLLSTTEW**	**A1,2,3,26 B8,27,4402,60**	**DR7**	**Tab.2,3,5**
1848	**LEDRDRSELSPLLLST**	**A1,2,3,26, B8,27,4402,60**	**DR7**	**Example VI**
	RSELSPLLL	A1		prediction
	ELSPLLLST	A2,A3		prediction
	DRDRSELSPL	A26,B27		prediction
	LEDRDRSEL	B08,B4402		prediction
1824	LEDRDRSEL	B60		Wong 2001
1547	**YLVAYQATVCARAQAPPPSWD**	**A2**	**DR1,4,7,11**	**Tab.2,3**
1822	YLVAYQATV	A2		Wentworth 1996
A1A7	**MSTNPKPQRKTKRNTNR**	**A11,B08,B27**		**Tab.5**

A3A7	PQRKTKRNTNR	B08,B27		Tab.5
	QRKTKRNTN	B08		prediction
	RKTKRNTNR	B2705		prediction
	MSTNPKPQR	A11		prediction
	MSTNPKPQK	A11		Wong 1998
A122EX	**LINTNGSWHINRTALNCNDSL**	**A2,2,3,B8**	**DR1,4,7,11**	**Tab.2,3**
A122	NGSWHINRTALNCNDSL	A2	DR1,4,7,11	Tab.2,3
	LINTNGSWHI	A2,3		prediction
	RTALNCNDSL	A2		prediction
1825	LINTNGSWHINRTALN	A2,3,B8		prediction
1826	SWHINRTALN	B8		prediction
A241	**TTILGIGTVLDQAET**	**A2,A3**	**DR1, 4**	**Tab.2,5**
	TTILGIGTV	A2		prediction
	TILGIGTVL	A3		prediction
B8B38	**FDSSVLCECYDAGAAWYE**	**A1,2,3,26**		**Tab.5**
B8	FDSSVLCECYDAGCA	A3,A26		Tab.5
	VLCECYDAGA	A2		prediction
B38	VVLCECYDAGAAWYE	A1		Tab.5
C70EX	**ARLIVFPDLGVRVCEKMALY**	**A2,A3,B27**		**Tab.5**
C64-C70	ARLIVFPDL	B*2705?,*2709?		Tab.5
1831	RLIVFPDLGV	A2		Gruener 2000
1832	RVCEKMALY	A3		Wong 1998
C92	**AFCSAMYVGDLCGSV**	**A2,B51**	**DR1,4**	**Tab.2,5**
C97	**GVLFGLAYFSMVGNW**	**A2,3,26, B2705,51**	**DR1,4,7**	**Tab.5**
C106	**TRVPYFVRAQGLIRA**	**A3,24, B7,B8,B2705**	**DR1,4,7**	**Tab.2,5**
C134	**TTLLFNILGGWVAAQ**	**A2**	**DR1, 7,11**	**Tab.2,5**
1823	LLFNILGGWV	A2		Bategay 1995

Example VII. HCV epitope hotspot Ipep 1426 contains at least HLA-A*0201 and several promiscuous class II T-cell epitopes

The major objective of this experiment was to compare the immunogenicity of the "hospot" Ipep 1426, which contains at least one HLA-A*0201 epitope (Ipep 1334) and 2 promiscuous class II epitopes (Ipeps 1006 and 1425), to the individual epitopes. To this end peripheral blood mononuclear cells (PBMC) from several healthy HLA-typed blood donors were stimulated in vitro either with 1426 or a mixture of 1334, 1006, 1425. Three rounds of

stimulation were performed resulting in oligoclonal T cell lines. Then, responses against all four peptides were assessed by interferon-gamma (IFN-γ) ELIspot analysis.

Peptide 1426, induces T cell responses similarly well as individual epitopes comprised within its sequence. In particular, CD8 positive T cells directed against the HLA-A*0201 restricted epitope 1334 were successfully generated.

Table 8: peptide induced IFN-γ secretion of oligoclonal T cell lines. Lines were generated from two HLA-typed healthy individuals by 3 rounds of in vitro priming with either peptide 1426 or a mixture of peptides 1006+1425+1334. The reactivity of CD4 and CD8 positive T cells in these lines was assessed by IFN-γ ELIspot ("+++" very strong, "++" strong, "+" significant, "-" no IFN-gamma secretion).

Donor HLA	**A*0201,** A*03, B7, B60; **DRB1*1501,** -B1*1302		A*0206, A*01, B27, B50; **DRB1*0401,** -B1*1402	
Peptide ID	**line raised against 1426**	**line raised against 1006+1425+1334**	**line raised against 1426**	**line raised against 1006+1425+1334**
1006	++	++	++	++
1425	+++	+++	+++	++
1334	+	+	-	-
1006+1425+1334	++	++	++	++
1426	+++	+++	+++	++
84 (HCV derived negative control)	-	-	-	-

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Claims:

1. Method for isolating Hepatitis C Virus peptides (HPs) which have a binding capacity to a MHC/HLA molecule or a complex comprising said HCV-peptide and said MHC/HLA molecule characterized by the following steps:

-providing a pool of HCV-peptide, said pool containing HCV-peptides which bind to said MHC/HLA molecule and HCV-peptides which do not bind to said MHC/HLA molecule,

-contacting said MHC/HLA molecule with said pool of HCV-peptides whereby a HCV-peptide which has a binding capacity to said MHC/HLA molecule binds to said MHC/HLA molecule and a complex comprising said HCV-peptide and said MHC/HLA molecule is formed,

-detecting and optionally separating said complex from the HCV-peptides which do not bind to said MHC/HLA molecule and

-optionally isolating and characterising the HCV-peptide from said complex.

2. Method for isolating HCV T cell epitopes which have a binding capacity to a MHC/HLA molecule or a complex comprising said epitope and said MHC/HLA molecule characterized by the following steps:

-providing a pool of HCV-peptides, said pool containing HCV-peptides which bind to a MHC/HLA molecule and HCV-peptides which do not bind to said MHC/HLA molecule,

-contacting said MHC/HLA molecule with said pool of HCV-peptides whereby a HCV-peptide which has a binding capacity to said MHC/HLA molecule binds to said MHC/HLA molecule and a complex comprising said HCV-peptide and said MHC/HLA molecule is formed,

-detecting and optionally separating said complex from the HCV-peptides which do not bind to said MHC/HLA molecule,

-optionally isolating and characterising the HCV-peptide from said complex,

-assaying said optionally isolated HCV-peptide or said complex in a T cell assay for T cell activation capacity and

-providing the optionally isolated HCV-peptide with a T cell activation capacity as HCV T cell epitope or as complex.

3. Method according to claim 1 or 2, characterized in that said pool of HCV-peptides is selected from the group consisting of a pool of peptides, especially overlapping peptides, a pool of protein fragments, a pool of modified peptides, a pool obtained from antigen-presenting cells, preferably in the form of total lysates or fractions thereof, especially fractions eluted from the surface or the MHC/HLA molecules of these cells, a pool comprised of fragments of cells, especially HCV-containing cells, tumor cells or tissues, especially from liver, a pool comprised of peptide libraries, pools of (poly)-peptides generated from recombinant DNA libraries, especially derived from pathogens or tumor cells, a pool of proteins and/or protein fragments from HCV or mixtures thereof.

4. Method according to any one of claims 1 to 3, characterized in that said MHC/HLA molecules are selected from HLA class I molecules, HLA class II molecules, non classical MHC/HLA and MHC/HLA-like molecules or mixtures thereof, or mixtures thereof.

5. Method according to any one of claims 1 to 4, characterized in that said characterising of the HCV-peptides of the complex is performed by using a method selected from the group consisting of mass spectroscopy, polypeptide sequencing, binding assays, especially SDS-stability assays, identification of HCV-peptides by determination of their retention factors by chromatography, especially HPLC, or other spectroscopic techniques, especially violet (UV), infra-red (IR), nuclear magnetic resonance (NMR), circular dichroism (CD) or electron spin resonance (ESR), or combinations thereof.

6. Method according to any one of claims 1 to 5, characterized in that it is combined with a cytokine secretion assay, preferably with an Elispot assay, an intracellular cytokine staining, FACS or an ELISA.

7. Method according to any one of claims 1 to 6, characterized in that said T cell assay comprises the mixing and incubation of said complex with isolated T cells and subsequent measuring cytokine secretion or proliferation of said isolated T cells.

8. Method according to any one of claims 1 to 6, characterized in that said T cell assay comprises measuring up-regulation of activation markers, especially CD69, CD38, or down-regulation of surface markers, especially CD3, CD8 or TCR.

9. Method according to any one of claims 1 to 8, characterized in that said T cell assay comprises measuring up-/down-regulation of mRNAs involved in T cell activation, especially by real-time RT-PCR.

10. Method according to any one of claims 1 to 8, characterized in that said T cell assay is selected from T cell assays measuring phosphorylation/de-phosphorylation of components downstream of the T cell receptor, especially p56 lck, ITAMS of the TCR and the zeta chain, ZAP70, LAT, SLP-76, fyn, and lyn, T cell assays measuring intracellular Ca^{++} concentration or activation of Ca^{++}-dependent proteins, T cell assays measuring formation of immunological synapses, T cell assays measuring release of effector molecules, especially perforin, granzymes or granulolysin or combinations of such T cell assays.

11. T cell epitopes identifyable by a method according to any one of claims 2 to 10, said T cell epitopes being selected from the group consisting of polypeptides A120-A124, B25-B30, B46-B48, B84-B92, C106, C113-C114, 1627, 1628, 1629, 1604, 1630, C97, 1547, B94-B98, A272-A276, B120, B122, C108, C134, C152, 1606, 1607, 1577, 1578, B50-52, 1623, C130, 1603, C96, C191, A216-A224, A242-A244, C92-C93, A174, B32-B38, B100-B102, C135, C162, 1618, 1622, 1624, 1546, 1556, A114, B58, B112-B118, B18-B22, C112, C116, C122, C127, C144, C159-C160, C174, 1558, 1581, C95, C129, C157-C158, A254-A258, 1605, C109, C161, 1547, 1555, 1558, 1559, 1560, 1563, 1592, 1605, 1616, 1621, 1623, 1625, 1649, 1650, 1651, 1652, 1654, 1655, 1656, 1545, 1552, 1557, 1615, 1617, 1631, 1632, 1641, 1647, 1653, A141, C114, C134, C135 and 1426.

12. HLA A0201 binding epitopes with T cell activating capacity identifyable by a method according to any one of claims 2 to 10 using HLA A0201 molecules as MHC/HLA molecules, said HLA A0201

binding epitopes being selected from the group consisting of polypeptides 1545, 1552, 1555, 1558, 1559, 1560, 1577, 1592, 1604, 1605, 1615, 1617, 1621, 1627, 1631, 1632, 1641, 1647, 1650, 1651, 1652, 1653, 1654, 1655 as specified in Table 1.

13. HLA-B*0702 binding epitopes with T cell activating capacity identifyable by a method according to any one of claims 2 to 10 using HLA-B*0702 molecules as MHC/HLA molecules, said HLA B*0702 binding epitopes being selected from the group consisting of polypeptides 1506, 1526, 1547, 1552, 1553, 1555, 1558, 1562, 1563, 1565, 1577, 1578, 1580, 1587, 1592, 1604, 1605, 1621, 1623, 1624, 1627, 1628, 1647, 1650, 1651, 1843 with sequence LPRRGPRL (contained in 1506) and 1838 with sequence SPGALVVGVI (contained in 1587) as minimal HLA-B*0702 epitopes.

14. Epitope or peptide according to any one of claims 11 to 13 characterized in that it further comprises 1 to 30, preferably 2 to 10, especially 2 to 6, naturally occurring amino acid residues, especially at the N-terminus, the C-terminus or at the N- and C-terminus.

15. Epitope or peptide according to any one of claims 11 to 14, characterized in that it further comprises a non-naturally occuring amino acid(s), preferably 1 to 1000, more preferred 2 to 100, especially 2 to 20 non-naturally occurring amino acid residues, at the N-terminus, the C-terminus or at the N- and C-terminus.

16. Use of an epitope or peptide according to any one of claims 11 to 14 for the preparation of a vaccine, especially of a HLA restricted vaccine, for treating or preventing hepatitis C virus (HCV) infections.

17. Vaccine for treating or preventing hepatitis C virus (HCV) infections comprising an epitope according to any one of claims 11 to 15.

18. HLA specific vaccine for treating or preventing hepatitis C virus (HCV) infections comprising an epitope or peptide according to any one of claims 11 to 15.

19. Vaccine as defined in any one of claims 16 to 18, characterized in that it further comprises an immunomodulating substance, preferably selected from the group consisting of polycationic substances, especially polycationic polypeptides, immunomodulating nucleic acids, especially deoxyinosine and/or deoxyuracile containing oligodeoxynucleotides, or mixtures thereof.

20. Vaccine as defined in any one of claims 16 to 19, characterized in that it further comprises a pharmaceutically acceptable carrier.

21. Vaccine as defined in any one of claims 16 to 20, characterized in that said epitope is provided in a form selected from peptides, peptide analogues, proteins, naked DNA, RNA, viral vectors, virus-like particles, recombinant/chimeric viruses, recombinant bacteria or dendritic cells pulsed with protein/peptide/RNA or transfected with DNA comprising the epitopes.

22. T cells, a T cell clone or a T cell population or preparation specifically recognizing an epitope or peptide according to any one of claims 11 to 15.

23. Use of T cells, a T cell clone or a T cell population or preparation according to claim 22 for identification of heteroclitic epitopes.

24. Use of T cells, a T cell clone or a T cell population or preparation according to claim 22 for the preparation of a composition for therapy of HCV patients.

25. Use of the peptides with formulae QRKTKRNTN or QRKTKRNT, or 1615, 1616, 1617 in particular 9meric peptides derived from the latter 3 peptides with formulae SAKSKFGYG, SAKSKYGYG, or SARSKYGYG as HLA-B*08 epitopes, especially for the preparation of a pharmaceutical preparation for a HLA-B*08 specific vaccine.

26. Use of the peptides with the formulae RKTKRNTNR as HLA-B*2705 epitope, especially for the preparation of a pharmaceut-

ical preparation for a HLA-B*2705 specific vaccine.

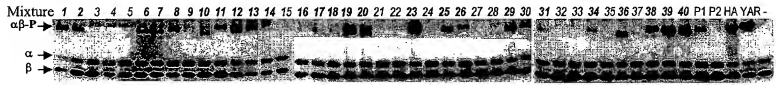
27. Use of the peptides with the formulae ARLIVFPDL as HLA-B*2705 and HLA-B*2709 specific vaccine.

28. Use of peptides as specified in Tab. 7, said peptides representing T-cell epitope hotspot and selected from the group of peptides 1835, 84EX, 87EX, 89EX, 1426, 1650, 1836, 1846, 1651, 1800, 1799, C114, 1827, C112, C114EX, 1827EX, 1798, 1604, 1829, 1579, 1624, 1848, 1547, A1A7, A122EX, A122, 1825, A241, B8B38, C70EX, C92, C97, C106, and C134.

Figure 1. HCV peptide array

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20
M21	A2	A4	A6	A8	A10	A12	A14	A16	A18	A20	A22	A24	A26	A28	A30	A32	A34	A36	1631	1632
M22	A38	A40	A42	A44	A46	A48	A50	A52	A54	A56	A58	A60	A62	A64	A66	A68	A70	A72	1624	1625
M23	A74	A76	A78	A80	A82	A84	A86	A88	A90	A92*	A94	A96	A98	A100	A102	A104	A106	A108	1577	1578
M24	A110	A112	A114	A116	A118	A120	A122	A124	A126	A128	A130	A132	A134	A136	A138	A140	A142	A144	1579	1580
M25	A146	A148	A150	A152	A154	A156	A158	A160	A162	A164	A166	A168	A170	A172	A174	A176	A178	A180	1547	1623
M26	A182	A184	A186	A188	A190	A192	A194	A196	A198	A200	A202	A204	A206	A208	A210	A212	A214	A216	1606	1607
M27	A218	A220	A222	A224	A226	A228	A230	A232	A234	A236	A238	A240	A242	A244	A246	A248	A250	A252	1626	1613
M28	A254	A256	A258	A260	A262	A264	A266*	A268	A270	A272	A274	A276	B2	B4	B6	B8	B10	B12	1604	1605
M29	B14	B16	B18	B20	B22	B24	B26	B28	B30	B32*	B34	B36	B38	B40	B42	B44	B46	B48	1618	1619
M30	B50	B52	B54	B56	B58	B60	B62	B64	B66	B68	B70	B72*	B74	B76	B78	B80	B82	B84	1559	1560
M31	B86	B88	B90	B92	B94	B96	B98	B100	B102	B104	B106	B108	B110	B112	B114	B116	B118	B120	B122	B124
M32	C2	C4	C6	C8	C10	C12	C14	C16	C18	C20	C22	C24	C26	C28	C30	C32	C34	C36	1614	1615
M33	C38	C40	C42	C44	C46	C47	C50	C52	C54	C56	C58	C60	C62	C64	C66	C68	C70	C72	1616	1617
M34	C74	C76	C78	C80	C82	C84	C85	C88	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101
M35	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120	PBS
M36	C121	C122	C123	C124	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	1620	1621
M37	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	PBS	PBS
M38	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	PBS	PBS
M39	C175	C176	C177	C178	C179	C180	C181	C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	PBS	PBS
M40	1629	1628	1630	1545	1581	1546	1622	1603	1557	1558	1556	1627	PBS	PBS	PBS	C193	C195	C197	PBS	PBS

Figure 2. Peptide pools that bind to DRB1*0401

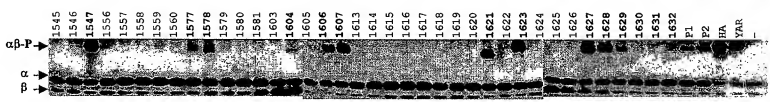


	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20
M21	A2	A4	A6	A8	A10	A12	A14	A16	A18	A20	A22	A24	A26	A28	A30	A32	A34	A36	1631	1632
M22	A38	A40	A42	A44	A46	A48	A50	A52	A54	A56	A58	A60	A62	A64	A66	A68	A70	A72	1624	1625
M23	A74	A76	A78	A80	A82	A84	A86	A88	A90	A92*	A94	A96	A98	A100	A102	A104	A106	A108	1577	1578
M24	A110	A112	A114	A116	A118	A120	A122	A124	A126	A128	A130	A132	A134	A136	A138	A140	A142	A144	1579	1580
M25	A146	A148	A150	A152	A154	A156	A158	A160	A162	A164	A166	A168	A170	A172	A174	A176	A178	A180	1547	1623
M26	A182	A184	A186	A188	A190	A192	A194	A196	A198	A200	A202	A204	A206	A208	A210	A212	A214	A216	1606	1607
M27	A218	A220	A222	A224	A226	A228	A230	A232	A234	A236	A238	A240	A242	A244	A246	A248	A250	A252	1626	1613
M28	A254	A256	A258	A260	A262	A264	A266*	A268	A270	A272	A274	A276	B2	B4	B6	B8	B10	B12	1604	1605
M29	B14	B16	B18	B20	B22	B24	B26	B28	B30	B32*	B34	B36	B38	B40	B42	B44	B46	B48	1618	1619
M30	B50	B52	B54	B56	B58	B60	B62	B64	B66	B68	B70	B72*	B74	B76	B78	B80	B82	B84	1559	1560
M31	B86	B88	B90	B92	B94	B96	B98	B100	B102	B104	B106	B108	B110	B112	B114	B116	B118	B120	B122	B124
M32	C2	C4	C6	C8	C10	C12	C14	C16	C18	C20	C22	C24	C26	C28	C30	C32	C34	C36	1614	1615
M33	C38	C40	C42	C44	C46	C47	C50	C52	C54	C56	C58	C60	C62	C64	C66	C68	C70	C72	1616	1617
M34	C74	C76	C78	C80	C82	C84	C85	C88	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101
M35	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120	PBS
M36	C121	C122	C123	C124	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	1620	1621
M37	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	PBS	PBS
M38	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	PBS	PBS
M39	C175	C176	C177	C178	C179	C180	C181	C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	PBS	PBS
M40	1629	1628	1630	1545	1581	1546	1622	1603	1557	1558	1556	1627	PBS	PBS	PBS	C193	C195	C197	PBS	PBS

Figure 3. Peptide pools that bind to DRB1*0404

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20
M21	A2	A4	A6	A8	A10	A12	A14	A16	A18	A20	A22	A24	A26	A28	A30	A32	A34	A36	1631	1632
M22	A38	A40	A42	A44	A46	A48	A50	A52	A54	A56	A58	A60	A62	A64	A66	A68	A70	A72	1624	1625*
M23	A74	A76	A78	A80	A82	A84	A86	A88	A90	A92*	A94	A96	A98	A100	A102	A104	A106	A108	1577	1578
M24	A110	A112	A114	A116	A118	A120	A122	A124	A126	A128	A130	A132	A134	A136	A138	A140	A142	A144	1579	1580
M25	A146	A148	A150	A152	A154	A156	A158	A160	A162	A164	A166	A168	A170	A172	A174	A176	A178	A180	1547	1623
M26	A182	A184	A186	A188	A190	A192	A194	A196	A198	A200	A202	A204	A206	A208	A210	A212	A214	A216	1606	1607
M27	A218	A220	A222	A224	A226	A228	A230	A232	A234	A236	A238	A240	A242	A244	A246	A248	A250	A252	1626	1613
M28	A254	A256	A258	A260	A262	A264	A266*	A268	A270	A272	A274	A276	B2	B4	B6	B8	B10	B12	1604	1605
M29	B14	B16	B18	B20	B22	B24	B26	B28	B30	B32*	B34	B36	B38	B40	B42	B44	B46	B48	1618	1619
M30	B50	B52	B54	B56	B58	B60	B62	B64	B66	B68	B70	B72*	B74	B76	B78	B80	B82	B84	1559	1560
M31	B86	B88	B90	B92	B94	B96	B98	B100	B102	B104	B106	B108	B110	B112	B114	B116	B118	B120	B122	B124
M32	C2	C4	C6	C8	C10	C12	C14	C16	C18	C20	C22	C24	C26	C28	C30	C32	C34	C36	1614	1615
M33	C38	C40	C42	C44	C46	C47	C50	C52	C54	C56	C58	C60	C62	C64	C66	C68	C70	C72	1616	1617
M34	C74	C76	C78	C80	C82	C84	C85	C88	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101
M35	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120	PBS
M36	C121	C122	C123	C124	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	1620	1621
M37	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	PBS	PBS
M38	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	PBS	PBS
M39	C175	C176	C177	C178	C179	C180	C181	C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	PBS	PBS
M40	1629	1628	1630	1545	1581	1546	1622	1603	1557	1558	1556	1627	PBS	PBS	PBS	C193	C195	C197	PBS	PBS

Figure 4. Individual peptides that bind to DRB1*0401



	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20
M21	A2	A4	A6	A8	A10	A12	A14	A16	A18	A20	A22	A24	A26	A28	A30	A32	A34	A36	**1631**	**1632**
M22	A38	A40	A42	A44	A46	A48	A50	A52	A54	A56	A58	A60	A62	A64	A66	A68	A70	A72	1624	1625
M23	A74	A76	A78	A80	A82	A84	A86	A88	A90	A92*	A94	**A96**	**A98**	**A100**	A102	**A104**	A106	A108	1577	**1578**
M24	A110	A112	A114	A116	A118	A120	A122	A124	A126	A128	A130	A132	A134	A136	A138	A140	A142	A144	1579	1580
M25	A146	A148	A150	A152	A154	A156	A158	A160	A162	A164	A166	A168	A170	A172	A174	A176	A178	A180	1547	1623
M26	A182	A184	A186	A188	A190	A192	A194	A196	A198	A200	**A202**	**A204**	**A206**	A208	A210	A212	A214	**A216**	**1606**	**1607**
M27	**A218**	**A220**	A222	A224	A226	A228	A230	A232	A234	A236	A238	A240	A242	**A244**	A246	A248	A250	A252	1626	1613
M28	A254	A256	A258	A260	A262	A264	A266*	A268	A270	**A272**	A274	A276	B2	B4	B6	B8	B10	B12	1604	1605
M29	B14	B16	B18	B20	B22	B24	B26	**B28**	**B30**	B32*	B34	B36	B38	B40	B42	B44	B46	B48	1618	1619
M30	B50	B52	B54	B56	B58	B60	**B62**	B64	B66	**B68**	B70	B72*	B74	B76	B78	B80	B82	B84	1559	1560
M31	B86	B88	B90	B92	B94	B96	B98	B100	B102	B104	B106	B108	B110	B112	B114	B116	B118	B120	B122	B124
M32	C2	C4	C6	C8	C10	C12	C14	C16	C18	C20	C22	C24	C26	C28	C30	C32	C34	C36	1614	1615
M33	C38	C40	C42	C44	C46	C47	C50	C52	C54	C56	C58	C60	C62	C64	C66	C68	C70	C72	1616	1617
M34	C74	C76	C78	C80	C82	C84	C85	C88	C90	C91	**C92**	**C93**	C94	**C95**	C96	**C97**	C98	C99	C100	C101
M35	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	**C113**	**C114**	C115	C116	C117	C118	C119	C120	PBS
M36	C121	C122	C123	**C124**	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	1620	1621
M37	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	PBS	PBS
M38	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	PBS	PBS
M39	C175	C176	C177	C178	C179	C180	C181	C182	C183	**C184**	C185	C186	C187	C188	C189	C190	C191	C192	PBS	PBS
M40	**1629**	**1628**	**1630**	1545	1581	1546	1622	1603	1557	1558	1556	**1627**	PBS	PBS	PBS	C193	C195	C197	PBS	PBS

Figure 5. Individual peptides that bind to DRB1*0404

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20
M21	A2	A4	A6	A8	A10	A12	A14	A16	A18	A20	A22	A24	A26	A28	A30	A32	A34	A36	1631	1632
M22	A38	A40	A42	A44	A46	A48	A50	A52	A54	A56	A58	A60	A62	A64	A66	A68	A70	A72	1624	1625*
M23	A74	A76	A78	A80	A82	A84	A86	A88	A90	A92*	A94	A96	A98	A100	A102	A104	A106	A108	1577	1578
M24	A110	A112	A114	A116	A118	A120	A122	A124	A126	A128	A130	A132	A134	A136	A138	A140	A142	A144	1579	1580
M25	A146	A148	A150	A152	A154	A156	A158	A160	A162	A164	A166	A168	A170	A172	A174	A176	A178	A180	1547	1623
M26	A182	A184	A186	A188	A190	A192	A194	A196	A198	A200	A202	A204	A206	A208	A210	A212	A214	A216	1606	1607
M27	A218	A220	A222	A224	A226	A228	A230	A232	A234	A236	A238	A240	A242	A244	A246	A248	A250	A252	1626	1613
M28	A254	A256	A258	A260	A262	A264	A266*	A268	A270	A272	A274	A276	B2	B4	B6	B8	B10	B12	1604	1605
M29	B14	B16	B18	B20	B22	B24	B26	B28	B30	B32*	B34	B36	B38	B40	B42	B44	B46	B48	1618	1619
M30	B50	B52	B54	B56	B58	B60	B62	B64	B66	B68	B70	B72*	B74	B76	B78	B80	B82	B84	1559	1560
M31	B86	B88	B90	B92	B94	B96	B98	B100	B102	B104	B106	B108	B110	B112	B114	B116	B118	B120	B122	B124
M32	C2	C4	C6	C8	C10	C12	C14	C16	C18	C20	C22	C24	C26	C28	C30	C32	C34	C36	1614	1615
M33	C38	C40	C42	C44	C46	C47	C50	C52	C54	C56	C58	C60	C62	C64	C66	C68	C70	C72	1616	1617
M34	C74	C76	C78	C80	C82	C84	C85	C88	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101
M35	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120	PBS
M36	C121	C122	C123	C124	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	1620	1621
M37	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	PBS	PBS
M38	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	PBS	PBS
M39	C175	C176	C177	C178	C179	C180	C181	C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	PBS	PBS
M40	1629	1628	1630	1545	1581	1546	1622	1603	1557	1558	1556	1627	PBS	PBS	PBS	C193	C195	C197	PBS	PBS

Figure 6. Individual peptides that bind to DRB1*0101

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20	
M21	A2	A4	A6	A8	A10	A12	A14	A16	A18	A20	A22	A24	A26	A28	A30	A32	A34	A36	1631	1632	
M22	A38	A40	A42	A44	A46	A48	A50	A52	A54	A56	A58	A60	A62	A64	A66	A68	A70	A72	1624	1625	
M23	A74	A76	A78	A80	A82	A84	A86	A88	A90	A92*	A94	A96	A98	A100	A102	A104	A106	A108	1577	1578	
M24	A110	A112	A114	A116	A118	A120	A122	A124	A126	A128	A130	A132	A134	A136	A138	A140	A142	A144	1579	1580	
M25	A146	A148	A150	A152	A154	A156	A158	A160	A162	A164	A166	A168	A170	A172	A174	A176	A178	A180	1547	1623	
M26	A182	A184	A186	A188	A190	A192	A194	A196	A198	A200	A202	A204	A206	A208	A210	A212	A214	A216	1606	1607	
M27	A218	A220	A222	A224	A226	A228	A230	A232	A234	A236	A238	A240	A242	A244	A246	A248	A250	A252	1226	1613	
M28	A254	A256	A258	A260	A262	A264	A266	A268	A270	A272	A274	A276	B2	B4	B6	B8	B10	B12	1604	1605	
M29	B14	B16	B18	B20	B22	B24	B26	B28	B30	B32*	B34	B36	B38	B40	B42	B44	B46	B48	1618	1619	
M30	B50	B52	B54	B56	B58	B60	B62	B64	B66	B68	B70	B72*	B74	B76	B78	B80	B82	B84	1559	1520	
M31	B86	B88	B90	B92	B94	B96	B98	B100	B102	B104	B106	B108	B110	B112	B114	B116	B118	B120	B122	B124	
M32	C2	C4	C6	C8	C10	C12	C14	C16	C18	C20	C22	C24	C26	C28	C30	C32	C34	C36	1614	1615	
M33	C38	C40	C42	C44	C46	C47	C50	C52	C54	C56	C58	C60	C62	C64	C66	C68	C70	C72	1616	1617	
M34	C74	C76	C78	C80	C82	C84	C85	C88	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101	
M35	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120	PBS	
M36	C121	C122	C123	C124	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	1620	1621	
M37	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	C157	PBS	
M38	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	PBS	PBS	
M39	C175	C176	C177	C178	C179	C180	C181	C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	PBS	PBS	
M40	1628	1629	1630	1545	1581	1546	1622	1603	1557	1558	1556	1627	PBS	PBS	PBS	PBS	C193	C195	C197	PBS	

Figure 7. Individual peptides that bind to DRB1*0701

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20
M21	A2	A4	A6	A8	A10	A12	A14	A16	A18	A20	A22	A24	A26	A28	A30	A32	A34	A36	1631	1632
M22	A38	A40	A42	A44	A46	A48	A50	A52	A54	A56	A58	A60	A62	A64	A66	A68	A70	A72	1624	1625
M23	A74	A76	A78	A80	A82	A84	A86	A88	A90	A92*	A94	A96	A98	A100	A102	A104	A106	A108	1577	1578
M24	A110	A112	A114	A116	A118	A120	A122	A124	A126	A128	A130	A132	A134	A136	A138	A140	A142	A144	1579	1580
M25	A146	A148	A150	A152	A154	A156	A158	A160	A162	A164	A166	A168	A170	A172	A174	A176	A178	A180	1547	1623
M26	A182	A184	A186	A188	A190	A192	A194	A196	A198	A200	A202	A204	A206	A208	A210	A212	A214	A216	1606	1607
M27	A218	A220	A222	A224	A226	A228	A230	A232	A234	A236	A238	A240	A242	A244	A246	A248	A250	A252	1626	1613
M28	A254	A256	A258	A260	A262	A264	A266*	A268	A270	A272	A274	A276	B2	B4	B6	B8	B10	B12	1604	1605
M29	B14	B16	B18	B20	B22	B24	B26	B28	B30	B32*	B34	B36	B38	B40	B42	B44	B46	B48	1618	1619
M30	B50	B52	B54	B56	B58	B60	B62	B64	B66	B68	B70	B72*	B74	B76	B78	B80	B82	B84	1559	1560
M31	B86	B88	B90	B92	B94	B96	B98	B100	B102	B104	B106	B108	B110	B112	B114	B116	B118	B120	B122	B124
M32	C2	C4	C6	C8	C10	C12	C14	C16	C18	C20	C22	C24	C26	C28	C30	C32	C34	C36	1614	1615
M33	C38	C40	C42	C44	C46	C47	C50	C52	C54	C56	C58	C60	C62	C64	C66	C68	C70	C72	1616	1617
M34	C74	C76	C78	C80	C82	C84	C85	C88	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101
M35	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120	PBS
M36	C121	C122	C123	C124	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	1620	1621
M37	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	PBS	PBS
M38	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	PBS	PBS
M39	C175	C176	C177	C178	C179	C180	C181	C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	PBS	PBS
M40	1629	1628	1630	1545	1581	1546	1622	1603	1557	1558	1556	1627	PBS	PBS	PBS	C193	C195	C197	PBS	PBS

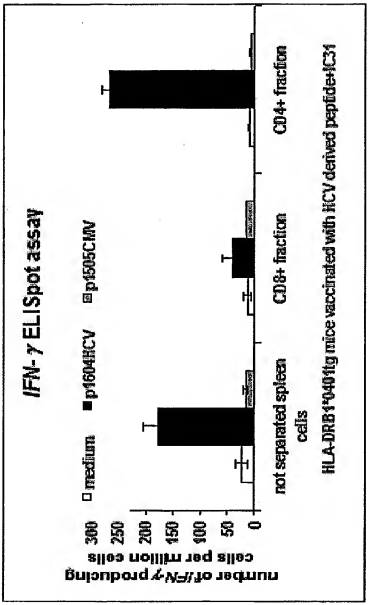
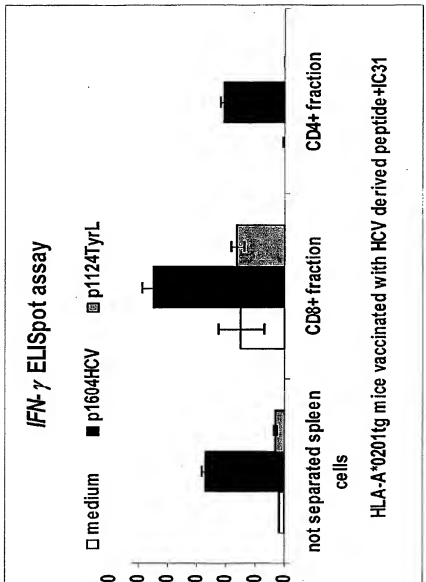

IFN-γ ELISpot assay
number of IFN-γ producing cells per million cells
300
250
200
150
100
50
0
medium
p1604HCV
p1605CMV
not separated spleen cells
CD8+ fraction
CD4+ fraction
HLA-DRB1*0401tg mice vaccinated with HCV derived peptide+IC31

Fig.8


IFN-γ ELISpot assay
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p1604HCV
p1124TyrL
number of IFN-γ producing cells per million cells
600
500
400
300
200
100
0
not separated spleen cells
CD8+ fraction
CD4+ fraction
HLA-A*0201tg mice vaccinated with HCV derived peptide+IC31

Fig.9

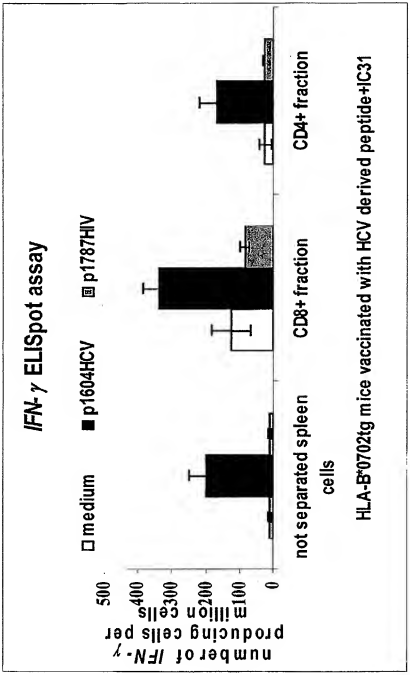
IFN-γ ELISpot assay
medium
p1604HCV
p1787HIV
number of IFN-γ producing cells per million cells
500
400
300
200
100
0
not separated spleen cells
CD8+ fraction
CD4+ fraction
HLA-B*0702tg mice vaccinated with HCV derived peptide+IC31

Fig.10